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OM protein - protein search, using sw model

Run on: March 24, 2003, 17:45:45 ; Search time 15 Seconds
(without alignments)
286.383 Million cell updates/sec

Title: US-10-031-403-1
Perfect score: 729
Sequence: 1 MAGELTPEEEAQYKKAFSAV.....DVDQDGRVNYEEFARMLAQE 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	726	99.6	146	3	US-08-963-409-1	Sequence 1, Appli
2	388.5	53.3	149	3	US-08-963-409-3	Sequence 3, Appli
3	384.5	52.7	149	3	US-08-963-409-4	Sequence 4, Appli
4	384.5	52.7	149	3	US-08-641-873-20	Sequence 20, Appl
5	376.5	51.6	642	2	US-08-818-253-2	Sequence 2, Appli
6	376.5	51.6	642	4	US-08-818-252-2	Sequence 2, Appli
7	376.5	51.6	652	2	US-08-818-253-4	Sequence 4, Appli
8	376.5	51.6	652	4	US-08-818-252-4	Sequence 4, Appli
9	373.5	51.2	642	2	US-08-818-253-6	Sequence 6, Appli
10	373.5	51.2	642	4	US-08-818-252-6	Sequence 6, Appli
11	373.5	51.2	656	2	US-08-818-253-8	Sequence 8, Appli
12	373.5	51.2	656	4	US-08-818-252-8	Sequence 8, Appli
13	373	51.2	152	3	US-08-963-409-5	Sequence 5, Appli
14	365.5	50.1	142	1	US-07-951-715A-24	Sequence 24, Appl
15	365.5	50.1	142	2	US-08-459-448A-24	Sequence 24, Appl
16	365.5	50.1	142	3	US-08-459-595A-24	Sequence 24, Appl
17	365.5	50.1	142	3	US-08-459-504B-24	Sequence 24, Appl
18	365.5	50.1	142	3	US-08-459-444-24	Sequence 24, Appl
19	365.5	50.1	142	4	US-09-547-422-24	Sequence 24, Appl
20	355.5	48.8	149	1	US-08-100-874-2	Sequence 2, Appli
21	348.5	47.8	145	4	US-08-720-625-5	Sequence 5, Appli
22	324.5	44.5	150	4	US-09-239-909-2	Sequence 2, Appli
23	305.5	41.9	150	4	US-09-239-909-4	Sequence 4, Appli
24	286.5	39.3	172	4	US-09-285-601-2	Sequence 2, Appli
25	256	35.1	160	2	US-08-602-941-1	Sequence 1, Appli
26	256	35.1	160	3	US-08-961-264-1	Sequence 1, Appli
27	256	35.1	160	4	US-09-442-099A-1	Sequence 1, Appli
28	254	34.8	163	2	US-08-698-805-8	Sequence 8, Appli
29	248	34.0	463	1	US-07-951-715A-25	Sequence 25, Appl
30	248	34.0	463	2	US-08-459-448A-25	Sequence 25, Appl
31	248	34.0	463	3	US-08-459-595A-25	Sequence 25, Appl
32	248	34.0	463	3	US-08-459-504B-25	Sequence 25, Appl
33	248	34.0	463	3	US-08-459-444-25	Sequence 0, Appli
34	248	34.0	463	4	US-09-547-422-25	Sequence 0, Appli
35	239.5	32.9	390	3	US-08-993-380-4	Sequence 4, Appli
36	237.5	32.6	408	1	US-07-951-715A-21	Sequence 21, Appl
37	237.5	32.6	408	2	US-08-459-448A-21	Sequence 21, Appl
38	237.5	32.6	408	3	US-08-459-595A-21	Sequence 21, Appl
39	237.5	32.6	408	3	US-08-459-504B-21	Sequence 21, Appl
40	237.5	32.6	408	3	US-08-459-444-21	Sequence 21, Appl
41	237.5	32.6	408	4	US-09-547-422-21	Sequence 21, Appl
42	237.5	32.6	464	1	US-07-951-715A-22	Sequence 22, Appl
43	237.5	32.6	464	2	US-08-459-448A-22	Sequence 22, Appl
44	237.5	32.6	464	3	US-08-459-595A-22	Sequence 22, Appl
45	237.5	32.6	464	3	US-08-459-504B-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-963-409-1
; Sequence 1, Application US/08963409
; Patent No. 6046315 issued 4/4/00
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: DISEASE ASSOCIATED CALMODULIN PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,409
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0418 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTTUT14
; CLONE: 2743380
US-08-963-409-1

Query Match 99.6%; Score 726; DB 3; Length 146;
Best Local Similarity 99.3%; Pred. No. 7.4e-69;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

good art, but not 100% match

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Qy      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60

Qy     61 DGEISFQEFLTAARKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120
          |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGEISFQEFLTAAKKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120

Qy    121 AMIREADVDQDGRVNYEEFARMLAQE 146
          |||||||||||||||||||||||||
Db    121 AMIREADVDQDGRVNYEEFARMLAQE 146


RESULT 2
US-08-963-409-3
; Sequence 3, Application US/08963409
; Patent No. 6046315
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  DISEASE ASSOCIATED CALMODULIN PROTEIN
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/963,409
;      FILING DATE:  Filed Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0418 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  149 amino acid
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  385234
US-08-963-409-3

  Query Match           53.3%;  Score 388.5;  DB 3;  Length 149;
  Best Local Similarity  52.1%;  Pred. No. 1.9e-33;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
          || :|| |: :::|:|||  | ||:|||  :|||  ::: |:| :|||:|: :|:|:|:||
Db      1 MADKLTEEQISEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEIDTDG 60

Qy     61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
          :| | | ||||  ||| :     |:|  ||| ||:||||:|: ||||  |  ||: |  |
Db     61 NGTIDFPEFLTLMARKLKDTDTEEELIEAFRVFDRDGDGYISADELRHVMTNLGEKLTNE 120

Qy    118 ELDAMIREADVDQDGRVNYEEFARML 143
          |:| ||||||:| ||::||||| :|:
Db    121 EVDEMIREADIDGDGQVNYEEFVKMM 146


RESULT 3
US-08-963-409-4
; Sequence 4, Application US/08963409
; Patent No. 6046315
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  DISEASE ASSOCIATED CALMODULIN PROTEIN
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/963,409
;      FILING DATE:  Filed Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0418 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  149 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1334203
US-08-963-409-4

  Query Match           52.7%;  Score 384.5;  DB 3;  Length 149;
  Best Local Similarity  52.1%;  Pred. No. 4.9e-33;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
          || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :|||:|: :|:|:|:||
Db      1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy     61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
          :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db     61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy    118 ELDAMIREADVDQDGRVNYEEFARML 143
          |:| ||||||:| ||:|||||| :|:
Db    121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 4
US-08-641-873-20
; Sequence 20, Application US/08641873
; Patent No. 6117976
;  GENERAL INFORMATION:
;    APPLICANT:  Neri, D.
;    APPLICANT:  Winter, GP.
```

```
;    APPLICANT:  de Lalla, C.
;    TITLE OF INVENTION:  Manufacture and use of polypeptides tagged
;    TITLE OF INVENTION:  using binding molecules
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/641,873
;      FILING DATE:  02-MAY-1996
;      CLASSIFICATION:  435
;      CLASSIFICATION:  G01N 33/68
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB94/02420
;      FILING DATE:  04-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9322772.6
;      FILING DATE:  04-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9405927.6
;      FILING DATE:  25-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  149 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-641-873-20

  Query Match             52.7%;  Score 384.5;  DB 3;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 4.9e-33;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  ||| | ||: | |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 5
US-08-818-253-2
; Sequence 2, Application US/08818253
; Patent No. 5998204
;  GENERAL INFORMATION:
;    APPLICANT:  Tsien, Roger Y.
;    APPLICANT:  Miyawaki, Atsushi
;    TITLE OF INVENTION:  FLUORESCENT PROTEIN SENSORS FOR
;    TITLE OF INVENTION:  DETECTION OF ANALYTES
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,253
;      FILING DATE:  14-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Ph.D., Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07257/043001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  642 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-818-253-2

  Query Match             51.6%;  Score 376.5;  DB 2;  Length 642;
  Best Local Similarity   51.4%;  Pred. No. 2.4e-31;
  Matches   75;  Conservative   32;  Mismatches   36;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           |  :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :|||:|: :|:|||:||
Db     230 MHDQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 289

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
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Db     290 NGTIYPPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 349

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     350 EVDEMIREADIDGDGQVNYEEFVQMM 375


RESULT 6
US-08-818-252-2
; Sequence 2, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
;  APPLICANT: Tsien, Roger Y.
;  APPLICANT: Miyawaki, Atsushi
;  TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
;  TITLE OF INVENTION: DETECTION OF ANALYTES
;  FILE REFERENCE: 07257/042001
;  CURRENT APPLICATION NUMBER: US/08/818,252B
;  CURRENT FILING DATE: 1997-03-14
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 642
;   TYPE: PRT
;   ORGANISM: Aequorea victoria
US-08-818-252-2

  Query Match             51.6%;  Score 376.5;  DB 4;  Length 642;
  Best Local Similarity   51.4%;  Pred. No. 2.4e-31;
  Matches   75;  Conservative   32;  Mismatches   36;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
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Db    230 MHDQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 289

Qy     61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
          :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db    290 NGTIYFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 349

Qy    118 ELDAMIREADVDQDGRVNYEEFARML 143
          |:| ||||||:| ||:|||||| :|:
Db    350 EVDEMIREADIDGDGQVNYEEFVQMM 375


RESULT 7
US-08-818-253-4
; Sequence 4, Application US/08818253
; Patent No. 5998204
;  GENERAL INFORMATION:
;    APPLICANT:  Tsien, Roger Y.
;    APPLICANT:  Miyawaki, Atsushi
;    TITLE OF INVENTION:  FLUORESCENT PROTEIN SENSORS FOR
;    TITLE OF INVENTION:  DETECTION OF ANALYTES
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,253
;      FILING DATE:  14-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Ph.D., Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07257/043001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  652 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-818-253-4

  Query Match             51.6%;  Score 376.5;  DB 2;  Length 652;
  Best Local Similarity   51.4%;  Pred. No. 2.5e-31;
  Matches   75;  Conservative   32;  Mismatches   36;  Indels    3;  Gaps    2;

Qy      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
          |  :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db    230 MHDQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 289

Qy     61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
          :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db    290 NGTIYFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 349

Qy    118 ELDAMIREADVDQDGRVNYEEFARML 143
          |:| ||||||:| ||:|||||| :|:
Db    350 EVDEMIREADIDGDGQVNYEEFVQMM 375


RESULT 8
US-08-818-252-4
; Sequence 4, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
;  APPLICANT: Tsien, Roger Y.
;  APPLICANT: Miyawaki, Atsushi
;  TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
;  TITLE OF INVENTION: DETECTION OF ANALYTES
;  FILE REFERENCE: 07257/042001
;  CURRENT APPLICATION NUMBER: US/08/818,252B
;  CURRENT FILING DATE: 1997-03-14
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 652
;   TYPE: PRT
;   ORGANISM: Aequorea victoria
US-08-818-252-4

  Query Match             51.6%;  Score 376.5;  DB 4;  Length 652;
  Best Local Similarity   51.4%;  Pred. No. 2.5e-31;
  Matches   75;  Conservative   32;  Mismatches   36;  Indels    3;  Gaps    2;

Qy      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
          |  :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db    230 MHDQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 289

Qy     61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
          :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db    290 NGTIYFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 349

Qy    118 ELDAMIREADVDQDGRVNYEEFARML 143
          |:| ||||||:| ||:|||||| :|:
Db    350 EVDEMIREADIDGDGQVNYEEFVQMM 375


RESULT 9
US-08-818-253-6
; Sequence 6, Application US/08818253
; Patent No. 5998204
;  GENERAL INFORMATION:
;    APPLICANT:  Tsien, Roger Y.
;    APPLICANT:  Miyawaki, Atsushi
;    TITLE OF INVENTION:  FLUORESCENT PROTEIN SENSORS FOR
;    TITLE OF INVENTION:  DETECTION OF ANALYTES
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,253
;      FILING DATE:  14-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Ph.D., Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07257/043001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  6:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  642 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-818-253-6

  Query Match             51.2%;  Score 373.5;  DB 2;  Length 642;
  Best Local Similarity   50.7%;  Pred. No. 5e-31;
  Matches   74;  Conservative   33;  Mismatches   36;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           |  :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db     230 MHDQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 289

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  :||  |  ||: |  |
Db     290 NGTIYFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAQLRHVMTNLGEKLTDE 349

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     350 EVDEMIREADIDGDGQVNYEEFVQMM 375


RESULT 10
US-08-818-252-6
; Sequence 6, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
;  APPLICANT: Tsien, Roger Y.
;  APPLICANT: Miyawaki, Atsushi
;  TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
;  TITLE OF INVENTION: DETECTION OF ANALYTES
;  FILE REFERENCE: 07257/042001
;  CURRENT APPLICATION NUMBER: US/08/818,252B
;  CURRENT FILING DATE: 1997-03-14
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 642
;   TYPE: PRT
;   ORGANISM: Aequorea victoria
US-08-818-252-6

  Query Match             51.2%;  Score 373.5;  DB 4;  Length 642;
  Best Local Similarity   50.7%;  Pred. No. 5e-31;
  Matches   74;  Conservative   33;  Mismatches   36;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           |  :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db     230 MHDQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 289

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  :||  |  ||: |  |
Db     290 NGTIYFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAQLRHVMTNLGEKLTDE 349

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     350 EVDEMIREADIDGDGQVNYEEFVQMM 375


RESULT 11
US-08-818-253-8
; Sequence 8, Application US/08818253
; Patent No. 5998204
;  GENERAL INFORMATION:
;    APPLICANT:  Tsien, Roger Y.
;    APPLICANT:  Miyawaki, Atsushi
;    TITLE OF INVENTION:  FLUORESCENT PROTEIN SENSORS FOR
;    TITLE OF INVENTION:  DETECTION OF ANALYTES
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,253
;      FILING DATE:  14-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Ph.D., Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07257/043001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  656 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-818-253-8

  Query Match             51.2%;  Score 373.5;  DB 2;  Length 656;
  Best Local Similarity   50.7%;  Pred. No. 5.2e-31;
  Matches   74;  Conservative   33;  Mismatches   36;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           |  :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db     246 MHDQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 305

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  :||  |  ||: |  |
Db     306 NGTIYFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAQLRHVMTNLGEKLTDE 365

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     366 EVDEMIREADIDGDGQVNYEEFVQMM 391


RESULT 12
US-08-818-252-8
; Sequence 8, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
;  APPLICANT: Tsien, Roger Y.
;  APPLICANT: Miyawaki, Atsushi
;  TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
;  TITLE OF INVENTION: DETECTION OF ANALYTES
;  FILE REFERENCE: 07257/042001
;  CURRENT APPLICATION NUMBER: US/08/818,252B
;  CURRENT FILING DATE: 1997-03-14
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 656
;   TYPE: PRT
;   ORGANISM: Aequorea victoria
US-08-818-252-8

  Query Match             51.2%;  Score 373.5;  DB 4;  Length 656;
  Best Local Similarity   50.7%;  Pred. No. 5.2e-31;
  Matches   74;  Conservative   33;  Mismatches   36;  Indels    3;  Gaps    2;
```

```
Qy      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
          |  :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db    246 MHDQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 305

Qy     61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
          :| | | ||||  ||| :     |::: ||| ||:||:|:|:  :||  |  ||: |  |
Db    306 NGTIYFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAQLRHVMTNLGEKLTDE 365

Qy    118 ELDAMIREADVDQDGRVNYEEFARML 143
          |:| ||||||:| ||:|||||| :|:
Db    366 EVDEMIREADIDGDGQVNYEEFVQMM 391


RESULT 13
US-08-963-409-5
; Sequence 5, Application US/08963409
; Patent No. 6046315
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  DISEASE ASSOCIATED CALMODULIN PROTEIN
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/963,409
;      FILING DATE:  Filed Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0418 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  152 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  825635
US-08-963-409-5

  Query Match             51.2%;  Score 373;  DB 3;  Length 152;
  Best Local Similarity   51.0%;  Pred. No. 8.2e-32;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    6;  Gaps    3;

Qy      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSD- 59
          || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:|
Db      1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADD 60

Qy     60 --GDGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPL 114
            |:| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |
Db     61 LPGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKL 120

Qy    115 PQEELDAMIREADVDQDGRVNYEEFARML 143
              ||:| |||||:| ||:|||||| :|:
Db    121 TDEEVDEMIREADIDGDGQVNYEEFVQMM 149


RESULT 14
US-07-951-715A-24
; Sequence 24, Application US/07951715A
; Patent No. 5625136
;  GENERAL INFORMATION:
;    APPLICANT:  Koziel, Michael G.
;    APPLICANT:  Desai, Nalini M.
;    APPLICANT:  Lewis, Kelly S.
;    APPLICANT:  Kramer, Vance C.
;    APPLICANT:  Warren, Gregory W.
;    APPLICANT:  Evola, Stephen V.
;    APPLICANT:  Crossland, Lyle D.
;    APPLICANT:  Wright, Martha S.
;    APPLICANT:  Merlin, Ellis J.
;    APPLICANT:  Launis, Karen L.
;    APPLICANT:  Rothstein, Steven J.
;    APPLICANT:  Bowman, Cindy G.
;    APPLICANT:  Dawson, John L.
;    APPLICANT:  Dunder, Erik M.
;    APPLICANT:  Pace, Gary M.
;    APPLICANT:  Suttie, Janet L.
;    TITLE OF INVENTION:  SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;    TITLE OF INVENTION:  INSECTICIDAL ACTIVITY IN MAIZE
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/951,715A
;      FILING DATE:  25-SEP-1992
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/772,027
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spruill, W. Murray
;      REGISTRATION NUMBER:  32,943
;      REFERENCE/DOCKET NUMBER:  S-18805/A/CGC 1577/CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8615
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  142 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..142
;      OTHER INFORMATION:  /note= "human calmodulin protein
;      OTHER INFORMATION:  sequence as shown in Figure 33."
US-07-951-715A-24

  Query Match             50.1%;  Score 365.5;  DB 1;  Length 142;
  Best Local Similarity   51.4%;  Pred. No. 4.6e-31;
  Matches   73;  Conservative   31;  Mismatches   35;  Indels    3;  Gaps    2;
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Qy       5 LTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGDGEI 64
           || |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||:| |
Db       1 LTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTI 60

Qy      65 SFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELDA 121
            | ||||  ||| :     |::: |||  |:||:|:|:  |||  |  ||: |  ||:|
Db      61 DFPEFLTMMARKMKDTDSEEEIREAFRVKDKDGNGYISAAELRHVMTNLGEKLTDEEVDE 120

Qy     122 MIREADVDQDGRVNYEEFARML 143
           |||||||:| ||:|||||| :|:
Db     121 MIREADIDGDGQVNYEEFVQMM 142


RESULT 15
US-08-459-448A-24
; Sequence 24, Application US/08459448A
; Patent No. 5859336
;  GENERAL INFORMATION:
;    APPLICANT:  Koziel, Michael G.
;    APPLICANT:  Desai, Nalini M.
;    APPLICANT:  Lewis, Kelly S.
;    APPLICANT:  Kramer, Vance C.
;    APPLICANT:  Warren, Gregory W.
;    APPLICANT:  Evola, Stephen V.
;    APPLICANT:  Crossland, Lyle D.
;    APPLICANT:  Wright, Martha S.
;    APPLICANT:  Merlin, Ellis J.
;    APPLICANT:  Launis, Karen L.
;    APPLICANT:  Rothstein, Steven J.
;    APPLICANT:  Bowman, Cindy G.
;    APPLICANT:  Dawson, John L.
;    APPLICANT:  Dunder, Erik M.
;    APPLICANT:  Pace, Gary M.
;    APPLICANT:  Suttie, Janet L.
;    TITLE OF INVENTION:  SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;    TITLE OF INVENTION:  INSECTICIDAL ACTIVITY IN MAIZE
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 5859336artis Corporation
;      STREET:  Patent & Trademark Dept., 520 White Plains
;      STREET:  Rd., POB 2005
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10591-9005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,448A
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/951,715
;      FILING DATE:  25-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/772,027
;      FILING DATE:  04-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pace, Gary M.
;      REGISTRATION NUMBER:  40403
;      REFERENCE/DOCKET NUMBER:  CGC 1577/CIP/DIV4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8582
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  142 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..142
;      OTHER INFORMATION:  /note= "human calmodulin protein
;      OTHER INFORMATION:  sequence as shown in Figure 33."
US-08-459-448A-24

  Query Match             50.1%;  Score 365.5;  DB 2;  Length 142;
  Best Local Similarity   51.4%;  Pred. No. 4.6e-31;
  Matches   73;  Conservative   31;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       5 LTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGDGEI 64
           || |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||:| |
Db       1 LTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTI 60

Qy      65 SFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELDA 121
            | ||||  ||| :     |::: |||  |:||:|:|:  |||  |  ||: |  ||:|
Db      61 DFPEFLTMMARKMKDTDSEEEIREAFRVKDKDGNGYISAAELRHVMTNLGEKLTDEEVDE 120

Qy     122 MIREADVDQDGRVNYEEFARML 143
           |||||||:| ||:|||||| :|:
Db     121 MIREADIDGDGQVNYEEFVQMM 142


Search completed: March 24, 2003, 17:46:28
Job time : 17 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 24, 2003, 17:43:00 ; Search time 40 Seconds
(without alignments)
486.365 Million cell updates/sec

Title: US-10-031-403-1
Perfect score: 729
Sequence: 1 MAGELTPEEEAQYKKAFSAV.....DVDQDGRVNYEEFARMLAQE 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	729	100.0	146	22	AAB67650	Amino acid sequenc
2	726	99.6	146	21	AAY87548	Human disease-asso
3	722	99.0	163	22	AAU87578	Novel central nerv
4	722	99.0	163	22	AAM43627	Human polypeptide
5	722	99.0	163	22	AAU19929	Novel human calciu
6	529	72.6	137	21	AAB58950	Breast and ovarian
7	384.5	52.7	149	11	AAR04583	Recombinant calmod
8	384.5	52.7	149	16	AAR78523	Human calmodulin p
9	384.5	52.7	149	21	AAG03832	Human secreted pro
10	384.5	52.7	149	22	AAU28050	Novel human secret
11	384.5	52.7	149	23	ABB57058	Mouse ischaemic co
12	384.5	52.7	149	23	AAU10388	Human calmodulin 1
13	380.5	52.2	149	22	ABB63876	Drosophila melanog
14	380.5	52.2	149	22	ABB66887	Drosophila melanog
15	380.5	52.2	149	22	ABB66889	Drosophila melanog
16	380.5	52.2	375	16	AAR78526	GST-calmodulin fus
17	379.5	52.1	148	23	ABB83067	Rat calmodulin ami
18	379.5	52.1	409	16	AAR78525	Protein A-calmodul
19	379.5	52.1	535	16	AAR78524	Maltose binding pr
20	376.5	51.6	416	23	ABB83069	Calcium sensor G85
21	376.5	51.6	642	19	AAW71645	Fluorescent calmod
22	376.5	51.6	652	19	AAW71646	Fluorescent calmod
23	373.5	51.2	642	19	AAW71647	Fluorescent calmod
24	373.5	51.2	656	19	AAW71648	Fluorescent calmod
25	370.5	50.8	151	9	AAP80162	Biosynthetic multi
26	365.5	50.1	143	23	ABB83312	Partial calmodulin
27	361.5	49.6	146	21	AAY50796	Human calmodulin/N
28	357.5	49.0	149	21	AAY50797	Human calmodulin/N
29	355.5	48.8	149	17	AAR81571	Potato calmodulin.
30	355.5	48.8	149	21	AAG22934	Arabidopsis thalia
31	355.5	48.8	182	21	AAG22933	Arabidopsis thalia
32	352.5	48.4	149	21	AAG09210	Arabidopsis thalia
33	352.5	48.4	149	21	AAG19559	Arabidopsis thalia
34	352.5	48.4	149	21	AAG36517	Arabidopsis thalia
35	352.5	48.4	149	21	AAG36788	Arabidopsis thalia
36	352.5	48.4	149	21	AAG38370	Arabidopsis thalia
37	352.5	48.4	149	21	AAG48103	Arabidopsis thalia
38	352.5	48.4	149	21	AAG48200	Arabidopsis thalia
39	352.5	48.4	151	21	AAG48102	Arabidopsis thalia
40	352.5	48.4	151	21	AAG48199	Arabidopsis thalia
41	352.5	48.4	159	21	AAG38438	Arabidopsis thalia
42	352.5	48.4	160	21	AAG36787	Arabidopsis thalia
43	352.5	48.4	182	21	AAG40532	Arabidopsis thalia
44	324.5	44.5	136	21	AAY77954	A. thaliana enviro
45	324.5	44.5	150	21	AAY95249	Soybean calmodulin

ALIGNMENTS

RESULT 1
AAB67650
ID AAB67650 standard; Protein; 146 AA.
XX
AC AAB67650;
XX
DT 29-MAY-2001 (first entry)
XX
DE Amino acid sequence of a human calmodulin-like skin protein.
XX
KW Human; calmodulin-like skin protein; CLSP; epidermal differentiation;
KW calcium-mediated signal pathway; epidermal proliferation; dry skin;
KW hyperkeratosis; parakeratosis; psoriasis; ichthyosis; neoplasia;
KW skin aging; skin damage.
XX
OS Homo sapiens.
XX
PN FR2796646-A1.
XX
PD 26-JAN-2001.
XX
PF 23-JUL-1999; 99FR-0009615.
XX
PR 23-JUL-1999; 99FR-0009615.
XX
PA (OREA) L'OREAL SA.
XX
PI Mehul B, Bernard D, Simonetti L;
XX
DR WPI; 2001-184569/19.
DR N-PSDB; AAF55621.
XX
PT New polypeptide isolated from human skin and having calcium fixing

```
PT   activity, useful for regulating epidermal proliferation and
PT   differentiation, e.g. in treatment of dry skin, psoriasis or neoplasia
PT   -
XX
PS   Claim 1; Page 20; 28pp; French.
XX
CC   The present sequence represents a human calmodulin-like skin protein
CC   (CLSP). CLSP is a calcium-mediated signal pathway modulator. CLSP
CC   polypeptides and polynucleotides are used cosmetically for regulating
CC   dysfunction of epidermal proliferation or differentiation (normal or
CC   pathological) and for treating dry skin, hyperkeratosis, parakeratosis,
CC   psoriasis, ichthyosis or neoplasia. They are especially used for
CC   treating skin aging and skin damage caused by exposure to ultraviolet
CC   radiation. They are also useful for preparing or purifying specific
CC   binding partners, especially specific antisera or monoclonal antibodies.
XX
SQ   Sequence   146 AA;

  Query Match             100.0%;  Score 729;  DB 22;  Length 146;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-67;
  Matches  146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60

Qy     61 DGEISFQEFLTAARKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120
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Qy    121 AMIREADVDQDGRVNYEEFARMLAQE 146
          |||||||||||||||||||||||||
Db    121 AMIREADVDQDGRVNYEEFARMLAQE 146


RESULT 2
AAY87548
ID   AAY87548 standard; Protein; 146 AA.
XX
AC   AAY87548;
XX
DT   18-JUL-2000  (first entry)
XX
DE   Human disease-associated calmodulin protein (DACP-1).
XX
KW   Disease-associated calmodulin protein; DACP-1; human; EF-hand;
KW   detection; quantitation; diagnosis; cancer; immune disorder;
KW   reproductive disorder; gynaecological; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   6
FT                   /note= "Phosphorylated by casein kinase II"
FT   Modified-site   18
FT                   /note= "Phosphorylated by casein kinase II"
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FT                   /note= "Phosphorylated by casein kinase II"
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FT   Domain          127..138
FT                   /note= "EF-hand domain"
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PN   US6046315-A.
XX
PD   04-APR-2000.
XX
PF   03-NOV-1997;   97US-0963409.
XX
PR   03-NOV-1997;   97US-0963409.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Hillman J,  Corley NC,  Shah P;
XX
DR   WPI; 2000-282708/24.
DR   N-PSDB; AAA10473.
XX
PT   New polynucleotide encoding a disease associated calmodulin protein
PT   (DACP-1) useful for diagnosing, preventing and treating cancer, immune
PT   disorders and reproductive disorders  -
XX
PS   Claim 1; Fig 1A-B; 27pp; English.
XX
CC   This sequence represents human disease-associated calmodulin protein
CC   (DACP-1). cDNA sequences encoding DACP-1 were initially isolated from
CC   a breast tumour cDNA library, the cDNA encoding this sequence
CC   being a consensus. Human DACP-1 has four EF-hand calcium-binding
CC   domains, and has chemical and structural homology with other calmodulin
CC   proteins from human, rat and Plasmodium falciparum. DACP-1 proteins and
CC   nucleotides are useful for the diagnosis, prevention, or treatment of
CC   cancers, immune disorders (e.g., AIDS) and reproductive disorders,
CC   including endometriosis. DACP-1 nucleotides are useful for detecting and
CC   quantitating gene expression in biopsied tissues in which expression of
CC   the protein may be correlated with a disease. Such a diagnostic assay may
CC   be used to distinguish between absence, presence, and overexpression of
CC   DACP-1, and to monitor regulation of DACP-1 levels during therapeutic
CC   intervention.  The nucleotide sequences are also useful in assays used to
CC   evaluate the efficacy of a particular therapeutic treatment regimen in
CC   animal studies, in clinical trials, or in monitoring the treatment of an
CC   individual patient. Nucleotides encoding DACP-1 are also useful in
CC   modulating DACP-1 expression e.g., in antisense therapy. DACP-1, and
CC   DACP-1 fragments and antibodies may be used in drug screening techniques.
CC   The antibodies may also be useful for the diagnosis of diseases
CC   associated with abnormal DACP-1 expression or activity.
XX
SQ   Sequence   146 AA;

  Query Match             99.6%;  Score 726;  DB 21;  Length 146;
  Best Local Similarity   99.3%;  Pred. No. 3.5e-67;
  Matches  145;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 DGEISFQEFLTAARKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120
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Db     61 DGEISFQEFLTAAKKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120

Qy    121 AMIREADVDQDGRVNYEEFARMLAQE 146
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Db    121 AMIREADVDQDGRVNYEEFARMLAQE 146


RESULT 3
AAU87578
ID   AAU87578 standard; Protein; 163 AA.
XX
AC   AAU87578;
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XX
DT 05-JUN-2002 (first entry)
XX
DE Novel central nervous system protein #488.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155318-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
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PR   05-DEC-2000; 2000US-0256719.
PR   06-DEC-2000; 2000US-0251479.
PR   08-DEC-2000; 2000US-0251856.
PR   08-DEC-2000; 2000US-0251868.
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PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-581633/65.
DR   N-PSDB; ABK43908.
XX
PT   New isolated nucleic acid encoding a protein for diagnosing,
PT   preventing, treating or ameliorating medical conditions and used as
PT   food additives or preservatives -
XX
PS   Claim 9; SEQ ID No 1096; 837pp; English.
XX
CC   The invention describes an isolated nucleic acid molecule (I) encoding a
CC   novel central nervous system protein. (I) and polypeptides (III) encoded
CC   by (I), are used to treat a medical conditions and in diagnosis of a
CC   pathological condition. Disorders which are diagnosed or treated include
CC   autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC   disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC   e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC   angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC   amylotrophic lateral sclerosis, infections caused by bacteria, viruses
CC   e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC   e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC   adenocarcinomas and irritable bowel syndrome, reproductive system
CC   disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC   and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC   leukaemia, disorders involving neovascularisation e.g. malignancies,
CC   respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC   acute kidney failure and blood related disorders e.g. myocardial
CC   infarction. The polypeptides can also be used to aid wound healing and
CC   epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC   maintain organs before transplantation, for supporting cell culture of
CC   primary tissues, to regenerate tissues and in chemotaxis. The
CC   polypeptides can also be used as a food additive or preservative to
CC   increase or decrease storage capabilities, fat content, lipid, protein,

  Query Match             99.0%;  Score 722;  DB 22;  Length 163;
  Best Local Similarity   98.6%;  Pred. No. 1e-66;
  Matches  144;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy      61 DGEISFQEFLTAARKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120
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Qy     121 AMIREADVDQDGRVNYEEFARMLAQE 146
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Db     138 AMIREADVDQDGRVNYEEFARMLAQE 163


RESULT 4
AAM43627
ID   AAM43627 standard; Protein; 163 AA.
XX
AC   AAM43627;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 305.
XX
KW   Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW   cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW   fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW   neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW   antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
KW   antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW   cardiovascular disorder; neurological disease; infection; human.
XX
OS   Homo sapiens.
XX
PN   WO200155308-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01309.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
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PR   14-AUG-2000; 2000US-0225757.
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PR   14-AUG-2000; 2000US-0225759.
PR   18-AUG-2000; 2000US-0226279.
PR   22-AUG-2000; 2000US-0226681.
PR   22-AUG-2000; 2000US-0226868.
PR   22-AUG-2000; 2000US-0227182.
PR   23-AUG-2000; 2000US-0227009.
PR   30-AUG-2000; 2000US-0228924.
PR   01-SEP-2000; 2000US-0229287.
PR   01-SEP-2000; 2000US-0229343.
PR   01-SEP-2000; 2000US-0229344.
PR   01-SEP-2000; 2000US-0229345.
PR   05-SEP-2000; 2000US-0229509.
PR   05-SEP-2000; 2000US-0229513.
PR   06-SEP-2000; 2000US-0230437.
PR   06-SEP-2000; 2000US-0230438.
PR   08-SEP-2000; 2000US-0231242.
PR   08-SEP-2000; 2000US-0231243.
PR   08-SEP-2000; 2000US-0231244.
PR   08-SEP-2000; 2000US-0231413.
PR   08-SEP-2000; 2000US-0231414.
PR   08-SEP-2000; 2000US-0232080.
PR   08-SEP-2000; 2000US-0232081.
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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-488781/53.
DR N-PSDB; AAI63933.
XX
PT New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX
PS Claim 11; SEQ ID NO 305; 664pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 163 AA;

Query Match 99.0%; Score 722; DB 22; Length 163;
Best Local Similarity 98.6%; Pred. No. 1e-66;
Matches 144; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      18 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDXDG 77

Qy      61 DGEISFQEFLTAARKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120
           |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db      78 DGEISFQEFLTAAKKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 137

Qy     121 AMIREADVDQDGRVNYEEFARMLAQE 146
           |||||||||||||||||||||||||
Db     138 AMIREADVDQDGRVNYEEFARMLAQE 163
```

RESULT 5
AAU19929
ID AAU19929 standard; Protein; 163 AA.
XX
AC AAU19929;
XX
DT 06-DEC-2001 (first entry)
XX
DE Novel human calcium-binding protein #38.
XX

KW Human; calcium-binding protein; calcium flux; neurological disease;
KW immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
KW virucide.
XX
OS Homo sapiens.
XX
PN WO200155304-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01302.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
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PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
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PR 29-SEP-2000; 2000US-0236368.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
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PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.

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PR   08-DEC-2000; 2000US-0251989.
PR   08-DEC-2000; 2000US-0251990.
PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465568/50.
DR   N-PSDB; AAS31614.
XX
PT   Isolated nucleic acid molecule encoding a calcium-binding protein is
PT   used in preventing, treating or ameliorating a medical condition  -
XX
PS   Claim 11; SEQ ID No 126; 542pp; English.
XX
CC   The present invention relates to the isolation of novel human
CC   calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic
CC   sequences encoding for these proteins. The sequences of the invention
CC   are useful in the diagnosis, prevention and/or prognosis of diseases
CC   associated with aberrant calcium flux. Such disorders include
CC   neurological diseases (e.g. amylotrophic lateral sclerosis, ALS),
CC   immune dysfunction (e.g. severe combined immunodeficiency, SCID),
CC   digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
CC   disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
CC   infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
CC   novel calcium-binding proteins are also useful as screening tools to
CC   identify antagonists and/or agonists that may enhance or inhibit
CC   activities mediated by calcium-binding proteins. The polynucleotides of
CC   the invention are also useful in gene therapy. AAU19892-AAU19969
CC   represent the novel human calcium-binding proteins.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   163 AA;

  Query Match            99.0%;  Score 722;  DB 22;  Length 163;
  Best Local Similarity  98.6%;  Pred. No. 1e-66;
  Matches  144;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      18 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDXDG 77

Qy      61 DGEISFQEFLTAARKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120
           |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db      78 DGEISFQEFLTAAKKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 137

Qy     121 AMIREADVDQDGRVNYEEFARMLAQE 146
           |||||||||||||||||||||||||
Db     138 AMIREADVDQDGRVNYEEFARMLAQE 163


RESULT 6
AAB58950
ID   AAB58950 standard; Protein; 137 AA.
XX
AC   AAB58950;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Breast and ovarian cancer associated antigen protein sequence SEQ ID 658.
XX
KW   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW   nootropic; neurpprotective; antiviral; antiallergic; hepatotropic;
KW   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW   antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW   Addison's disease; allergy; autoimmune haemolytic anaemia;
KW   autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW   multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW   cardiovascular disorder; wound healing; neurological disease.
XX
OS   Homo sapiens.
XX
PN   WO200055173-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05881.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-611515/58.
DR   N-PSDB; AAF21853.
XX
PT   New human breast and ovarian cancer associated gene sequences and the
PT   polypeptides encoded by these genes, useful in the prevention,
PT   treatment and diagnosis of cancer, immune disorders, cardiovascular
PT   disorders and neurological diseases -
XX
PS   Claim 11; Page 1104-1105; 1299pp; English.
XX
CC   Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC   proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC   associated with breast and ovarian cancer. Included in the invention are
CC   sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC   isolation and characterisation of the DNA and protein sequences of the
CC   invention. The breast and ovarian cancer associated DNA, protein, agonist
CC   or antagonist sequences exhibit cytostatic; immunosuppressive;
CC   nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
CC   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
CC   antibacterial; antifungal; antiparasitic and cardiant activity. The
CC   polynucleotide and protein sequences are used in the diagnosis of cancer,
CC   particularly breast and ovarian cancer. The nucleic acid sequences,
CC   proteins, agonists and agonists may also be used in the diagnosis,
CC   prevention and treatment of immune disorders e.g. Addison's disease,
CC   allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC   diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC   arthritis and ulcerative colitis; cardiovascular disorders such as
CC   myocardial ischaemias; wound healing; neurological diseases such as
CC   cerebral anoxia and epilepsy; and infectious diseases.
XX
SQ   Sequence   137 AA;

  Query Match            72.6%;  Score 529;  DB 21;  Length 137;
  Best Local Similarity  96.4%;  Pred. No. 7.2e-47;
  Matches  107;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      18 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDXDG 77

Qy      61 DGEISFQEFLTAARKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLG 111
           ||||||||||||| ||||||||| |||||||||||||||||||||||||||
Db      78 DGEISFQEFLTAAXKARAGLEDLXVAFRAFDQDGDGHITVDELRRAXAGLG 128


RESULT 7
AAR04583
ID   AAR04583 standard; protein; 149 AA.
XX
AC   AAR04583;
XX
DT   27-SEP-1990  (first entry)
XX
DE   Recombinant calmodulin.
XX
KW   Calmodulin.
XX
OS   Rattus rattus.
```

```
XX
PN   JP02092286-A.
XX
PD   03-APR-1990.
XX
PF   30-SEP-1988;   88JP-0246239.
XX
PR   30-SEP-1988;   88JP-0246239.
XX
PA   (KIRI ) KIRIN BREWERY KK.
XX
DR   WPI; 1990-144900/19.
DR   N-PSDB; AAQ04331.
XX
PT   Calmodulin prepn. - by culturing transformed E. coli.
XX
PS   Disclosure; ; p; Japanese.
XX
CC   The recombinant calmodulin is produced by cloning the gene into an
CC   expression vector and culturing to produce the protein.
CC   See also AAQ04332-4.
XX
SQ   Sequence   149 AA;

  Query Match             52.7%;  Score 384.5;  DB 11;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 6.7e-32;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
          || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db      1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy     61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
          :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db     61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy    118 ELDAMIREADVDQDGRVNYEEFARML 143
          |:| ||||||:| ||:|||||| :|:
Db    121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 8
AAR78523
ID   AAR78523 standard; Protein; 149 AA.
XX
AC   AAR78523;
XX
DT   31-JAN-1996  (first entry)
XX
DE   Human calmodulin protein.
XX
KW   Human; calmodulin; fibrosarcoma cell; primer; PCR; amplification;
KW   maltose; protein A; glutathione-S-transferase; fusion protein; activity;
KW   phosphodiesterase activating method; binding protein; inhibitor.
XX
OS   Homo sapiens.
XX
PN   JP07126297-A.
XX
PD   16-MAY-1995.
XX
PF   05-NOV-1993;   93JP-0299041.
XX
PR   05-NOV-1993;   93JP-0299041.
XX
PA   (SAGA ) SAGAMI CHEM RES CENTRE.
XX
DR   WPI; 1995-212960/28.
DR   N-PSDB; AAQ95549.
XX
PT   Fusion of calmodulin (CAM) with specific binding peptide - has same
PT   activity as CAM, useful for screening for CAM inhibitors, measuring
PT   CAM binding protein activity, etc.
XX
PS   Examples; Page 5-6; 12pp; Japanese.
XX
CC   The amino acid sequence of the human calmodulin cDNA clone pKA1-CAM.
CC   The clone was isolated from the human fibrosarcoma cell line HT-1080
CC   using primers AAQ95553-4 to PCR amplify the coding region.  The coding
CC   region of the gene was inserted into the plasmids pMAL(RTM)-2, pRIT2T
CC   and pGEX-5X-1 to generate plasmids pMALCAM (AAQ95550), pPACAM (AAQ95551)
CC   and pGSTCAM (AAQ95552) respectively.  These plasmids express maltose-
CC   (AAR78524), protein A- (AAR78525) and
CC   glutathione-S-transferase-calmodulin (AAR78526) fusion proteins,
CC   respectively.  The fusion proteins produced retain the same activity as
CC   calmodulin as measured by the phosphodiesterase activating method.  The
CC   fusion protein, which can be obtained at high purity, can be used to
CC   isolate calmodulin binding proteins, measure their activity and screen
CC   for calmodulin inhibitors.
XX
SQ   Sequence   149 AA;

  Query Match             52.7%;  Score 384.5;  DB 16;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 6.7e-32;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
          || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db      1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy     61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
          :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db     61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy    118 ELDAMIREADVDQDGRVNYEEFARML 143
          |:| ||||||:| ||:|||||| :|:
Db    121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 9
AAG03832
ID   AAG03832 standard; Protein; 149 AA.
XX
AC   AAG03832;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein, SEQ ID NO: 7913.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
DR   N-PSDB; AAC03838.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 13; SEQ ID 7913; 71pp + CD-ROM; English.
XX
CC   The present sequence is a polypeptide encoded by one of a large number
```

```
CC   of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC   were prepared from total human RNAs or polyA+ RNAs derived from 30
CC   different tissues. EST sequences usually correspond mainly to the 3'
CC   untranslated region (UTR) of the mRNA because they are often obtained
CC   from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC   isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC   those cases where longer cDNA sequences have been obtained, the full 5'
CC   UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC   ends and can therefore be used to obtain full length cDNAs and genomic
CC   DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC   chromosome mapping procedures. They are used to obtain upstream
CC   regulatory sequences and to design expression and secretion vectors.
XX
SQ   Sequence   149 AA;

  Query Match           52.7%;  Score 384.5;  DB 21;  Length 149;
  Best Local Similarity 52.1%;  Pred. No. 6.7e-32;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :     |::: ||| ||:||:|:|:  ||| | ||: | |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 10
AAU28050
ID   AAU28050 standard; Protein; 149 AA.
XX
AC   AAU28050;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Novel human secretory protein, Seq ID No 219.
XX
KW   Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
KW   ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
KW   transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
KW   amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
KW   ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KW   gut protection; lung; liver fibrosis; immune deficiency; infection;
KW   severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KW   multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KW   fertility; analgesic; pain; antigen.
XX
OS   Homo sapiens.
XX
PN   WO200166689-A2.
XX
PD   13-SEP-2001.
XX
PF   05-MAR-2001; 2001WO-US04942.
XX
PR   07-MAR-2000; 2000US-0519705.
PR   19-MAY-2000; 2000US-0574454.
PR   17-JUN-2000; 2000US-0596193.
PR   14-JUL-2000; 2000US-0616847.
PR   19-SEP-2000; 2000US-0665363.
PR   20-OCT-2000; 2000US-0693267.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
PI   Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
XX
DR   WPI; 2001-589934/66.
DR   N-PSDB; AAS44950.
XX
PT   Novel polypeptides and nucleic acids obtained from cDNA libraries
PT   prepared from various human tissues, for diagnosis and treatment of
PT   cancer, neurological, inflammatory, and autoimmune disorders -
XX
PS   Example 3; SEQ ID No 219; 107pp; English.
XX
CC   The invention relates to novel isolated human secreted polypeptides (I)
CC   and polynucleotides (II). (I) and (II) are useful for treating
CC   inflammatory conditions such as arthritis, nephritis, Crohn's disease,
CC   ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
CC   involved in increasing haematopoiesis, stem cell survival, bone growth
CC   and remodeling. (I), (II) and modulators of (II) are useful for
CC   prophylaxis or treatment of one or more cancers. (II) is also useful for
CC   creating transgenic animals useful for studying the in vivo activities of
CC   the polypeptide as well as for studying modulators of the polypeptides.
CC   (I) induces the proliferation of neural cells and regeneration of nerve
CC   and brain tissue and is useful for the treatment of central and
CC   peripheral nervous system diseases and neuropathies, such as Alzheimer's,
CC   Parkinson's disease, Huntington's disease, and amyotrophic lateral
CC   sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
CC   activity, regulation of haematopoiesis and is useful for treating myeloid
CC   or lymphoid cell disorders, platelet disorders such as thrombocytopenia
CC   and for regeneration of bone, cartilage, tendon, ligament and/or nerve
CC   tissue growth, and in tissue repair, healing of burns, incisions,
CC   ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
CC   disorders, or periodontal disease. Furthermore, (I) is also useful for
CC   gut protection or regeneration and treatment of lung or liver fibrosis,
CC   reperfusion injury in various tissues, various immune deficiencies and
CC   disorders including severe combined immunodeficiency (SCID), bacterial or
CC   fungal infections, autoimmune disorders e.g. multiple sclerosis,
CC   rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
CC   reactions and conditions, such as asthma or other respiratory problems.
CC   In addition, (I) affects biorhythms or circadian cycles of rhythms,
CC   fertility, metabolism, catabolism, anabolism, storage or elimination of
CC   dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
CC   analgesic effects or other pain reducing effects, immunoglobulin like
CC   activity and can act as an antigen in a vaccine composition to raise an
CC   immune response. AAU28020-AAU28395 represent novel human secreted protein
CC   amino acid sequences of the invention.
XX
SQ   Sequence   149 AA;

  Query Match           52.7%;  Score 384.5;  DB 22;  Length 149;
  Best Local Similarity 52.1%;  Pred. No. 6.7e-32;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :     |::: ||| ||:||:|:|:  ||| | ||: | |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 11
ABB57058
ID   ABB57058 standard; Protein; 149 AA.
XX
AC   ABB57058;
XX
DT   07-MAR-2002  (first entry)
XX
DE   Mouse ischaemic condition related protein sequence SEQ ID NO:112.
XX
KW   Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW   vasospastic ischaemia; ischaemic condition; ischaemic disease.
```

```
XX
OS   Mus musculus.
XX
PN   WO200188188-A2.
XX
PD   22-NOV-2001.
XX
PF   18-MAY-2001; 2001WO-JP04192.
XX
PR   18-MAY-2000; 2000JP-0145977.
XX
PA   (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI   Ishikawa K,  Asai S,  Takahashi Y,  Nagata T,  Ishii Y;
XX
DR   WPI; 2002-034733/04.
DR   N-PSDB; ABI99274.
XX
PT   Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT   expression levels of particular genes defined in the specification or
PT   by determining the expression profile of a gene group comprising these
PT   genes -
XX
PS   Claim 2; Page 322; 2690pp; English.
XX
CC   The present invention describes a method for examining ischaemic
CC   conditions, comprising measuring the expression levels of particular
CC   genes (I) in a test sample or determining the expression profile of a
CC   gene group in the sample comprising genes selected from (I). The method
CC   is useful for examining the ischaemic condition (e.g. compressive
CC   ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC   expression levels of particular genes (ABI99202 to ABI99912, encoding
CC   the protein sequences in ABB57020 to ABB57374) or by determining the
CC   expression profile of a gene group comprising these genes. The
CC   expression levels or expression profiles produced by these genes are
CC   used as an indicator when screening for ischaemic condition-improving
CC   drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
CC   represent PCR primers for a mouse ischaemic condition related sequence,
CC   which are used in the exemplification of the present invention.
XX
SQ   Sequence   149 AA;

  Query Match             52.7%;  Score 384.5;  DB 23;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 6.7e-32;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 12
AAU10388
ID   AAU10388 standard; Protein; 149 AA.
XX
AC   AAU10388;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Human calmodulin 1 (CALM1).
XX
KW   Calmodulin 1; CALM1; human; single nucleotide polymorphism; SNP;
KW   haplotyping; SCYA3; Alzheimer's disease; drug screening;
KW   calcium-dependent signal transduction.
XX
OS   Homo sapiens.
XX
PN   WO200179218-A2.
XX
PD   25-OCT-2001.
XX
PF   09-APR-2001; 2001WO-US11509.
XX
PR   12-APR-2000; 2000US-196340P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Chew A,  Choi JY,  Koshy B,  Stephens JC;
XX
DR   WPI; 2002-049190/06.
DR   N-PSDB; AAS17569, AAS17570.
XX
PT   New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in
PT   expressing CALM1 protein for use in screening for candidate drugs to
PT   treat diseases related to CALM1 activity such as Alzheimer's disease. -
XX
PS   Disclosure; Fig 4; 82pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising a
CC   sequence selected from a polymorphic variant of calmodulin 1 (CALM1).
CC   The polymorphic variant comprises an CALM1 isogene defined by a
CC   haplotype selected from haplotypes 1-21 given in the specification.
CC   The polymorphisms are useful for studying the biological function of
CC   CALM1 as well as in identifying drugs targeting this protein for the
CC   treatment of a disorder related to its abnormal expression or function.
CC   The polymorphic variants may also be used in screening for compounds
CC   targeting CALM1 to treat a specific condition or disease predicted to
CC   be associated with CALM1 activity. Establishing CALM1 haplotype or
CC   haplotype pair of an individual is useful for improving the efficiency
CC   and reliability of several steps in the discovery and development of
CC   drugs for treating diseases associated with SCYA3 activity, e.g.
CC   Alzheimer's disease and diseases involving defects in calcium-dependent
CC   signal transduction. Haplotyping the CALM1 gene in an individual is
CC   also useful in the design of clinical trials of candidate drugs for
CC   treating a specific condition or disease predicted to be associated
CC   with CALM1 activity. The present sequence represents the amino acid
CC   sequence of human CALM1.
XX
SQ   Sequence   149 AA;

  Query Match             52.7%;  Score 384.5;  DB 23;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 6.7e-32;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 13
ABB63876
ID   ABB63876 standard; Protein; 149 AA.
XX
AC   ABB63876;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 18420.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
```

```
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL07979.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Disclosure; SEQ ID NO 18420; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   149 AA;

  Query Match             52.2%;  Score 380.5;  DB 22;  Length 149;
  Best Local Similarity   51.0%;  Pred. No. 1.7e-31;
  Matches   76;  Conservative   31;  Mismatches   39;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:| |:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARMLAQE 146
           |:| ||||||:| ||:||||||  |:  :
Db     121 EVDEMIREADIDGDGQVNYEEFVTMMTSK 149


RESULT 14
ABB66887
ID   ABB66887 standard; Protein; 149 AA.
XX
AC   ABB66887;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 27453.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL10990.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Disclosure; SEQ ID NO 27453; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   149 AA;

  Query Match             52.2%;  Score 380.5;  DB 22;  Length 149;
  Best Local Similarity   51.0%;  Pred. No. 1.7e-31;
  Matches   76;  Conservative   31;  Mismatches   39;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:| |:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARMLAQE 146
           |:| ||||||:| ||:||||||  |:  :
Db     121 EVDEMIREADIDGDGQVNYEEFVTMMTSK 149


RESULT 15
ABB66889
ID   ABB66889 standard; Protein; 149 AA.
XX
AC   ABB66889;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 27459.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
```

PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL10992.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 27459; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 149 AA;

Query Match 52.2%; Score 380.5; DB 22; Length 149;
Best Local Similarity 51.0%; Pred. No. 1.7e-31;
Matches 76; Conservative 31; Mismatches 39; Indels 3; Gaps 2;

```
Qy      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
          || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db      1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy     61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
          :| | | ||||  ||| :     |::: ||| ||:||:| |:  |||  |  ||: |  |
Db     61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy    118 ELDAMIREADVDQDGRVNYEEFARMLAQE 146
          |:| ||||||:| ||:||||||  |:  :
Db    121 EVDEMIREADIDGDGQVNYEEFVTMMTSK 149
```

Search completed: March 24, 2003, 17:44:07
Job time : 41 secs

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 24, 2003, 17:44:35 ; Search time 19 Seconds
(without alignments)
738.717 Million cell updates/sec

Title: US-10-031-403-1
Perfect score: 729
Sequence: 1 MAGELTPEEEAQYKKAFSAV.....DVDQDGRVNYEEFARMLAQE 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	388.5	53.3	148	1	MCXAM	calmodulin - sea a
2	388.5	53.3	149	1	MCZQF	calmodulin - malar
3	385.5	52.9	148	1	MCSW	calmodulin - scall
4	384.5	52.7	149	1	MCHU	calmodulin [valida
5	384.5	52.7	149	1	MCRT	calmodulin [valida
6	384.5	52.7	149	1	MCCH	calmodulin - chick
7	384.5	52.7	149	1	I51202	calmodulin - duck
8	384.5	52.7	149	2	JC1305	calmodulin - Japan
9	384.5	52.7	149	2	I51402	calmodulin - Afric
10	384.5	52.7	149	2	S37707	calmodulin - mouse
11	383.5	52.6	147	1	MCJZR	calmodulin - sea p
12	382.5	52.5	149	1	MCEE	calmodulin - elect
13	380.5	52.2	148	1	MCAZS	calmodulin - sea s
14	380.5	52.2	149	1	MCFF	calmodulin [valida
15	380.5	52.2	149	1	MCGAC	calmodulin - Calif
16	379.5	52.1	148	1	MCBO	calmodulin [valida
17	379.5	52.1	148	1	MCON	calmodulin - salmo
18	379.5	52.1	149	2	T31737	hypothetical prote
19	378.5	51.9	148	1	MCSFCU	calmodulin - sea c
20	378.5	51.9	149	2	I49567	calmodulin - mouse
21	375.5	51.5	148	1	MCLQ	calmodulin - migra
22	374.5	51.4	148	1	MCRB	calmodulin - rabbi
23	373.5	51.2	149	2	S53019	calmodulin - Macro
24	371.5	51.0	141	2	S02690	calmodulin A - sea
25	371.5	51.0	149	1	MCUTC	calmodulin - Trypa
26	370.5	50.8	149	1	MCTE	calmodulin - Tetra
27	370.5	50.8	149	1	MCUTG	calmodulin - Trypa
28	370.5	50.8	149	2	JC1309	calmodulin - Stylo
29	370.5	50.8	149	2	A48111	calmodulin C - Try
30	370.5	50.8	149	2	S28954	calmodulin - Tetra
31	369.5	50.7	163	1	MCKM	calmodulin - Chlam
32	367.5	50.4	148	1	MCMRP	calmodulin - cornu
33	367.5	50.4	149	1	MCPP	calmodulin - Param
34	365.5	50.1	149	1	MCUMAK	calmodulin - Achly
35	365.5	50.1	151	1	MCDO	calmodulin - slime
36	364.5	50.0	148	1	MCEG	calmodulin - Eugle
37	363.5	49.9	149	1	MCCHM	calmodulin, striat
38	358.5	49.2	148	2	JC1094	calmodulin - rice
39	358.5	49.2	149	1	MCBH	calmodulin - barle
40	358.5	49.2	149	1	MCAA	calmodulin - alfal
41	358.5	49.2	149	2	S24952	calmodulin 1 (clon
42	358.5	49.2	149	2	S51933	calmodulin cam2 -
43	357.5	49.0	148	1	MCSP	calmodulin - spina
44	357.5	49.0	149	1	MCHUNB	calmodulin-related
45	355.5	48.8	138	2	S02691	calmodulin B - sea

ALIGNMENTS

RESULT 1
MCXAM
calmodulin - sea anemone (Metridium senile) (tentative sequence)
N;Alternate names: modulator protein
C;Species: Metridium senile (brown sea anemone, frilled sea anemone)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 24-Nov-1999
C;Accession: A90223; A03023
R;Takagi, T.; Nemoto, T.; Konishi, K.; Yazawa, M.; Yagi, K.
Biochem. Biophys. Res. Commun. 96, 377-381, 1980
A;Title: The amino acid sequence of the calmodulin obtained from sea anemone (Metridi
A;Reference number: A90223; MUID:81062446; PMID:6108109
A;Accession: A90223
A;Molecule type: protein
A;Residues: 1-148 <TAK>
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; methylated amin
F;7-39/Domain: calmodulin repeat homology <EF1>
F;43-75/Domain: calmodulin repeat homology <EF2>
F;80-112/Domain: calmodulin repeat homology <EF3>
F;116-148/Domain: calmodulin repeat homology <EF4>
F;1/Modified site: blocked amino end (Ala) #status experimental
F;20,22,24,26,31/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status predicted
F;56,58,60,62,67/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status predicted
F;93,95,97,99,104/Binding site: calcium (Asp, Asp, Asp, Phe, Glu) #status predicted
F;115/Modified site: N6,N6,N6-trimethyllysine (Lys) #status experimental
F;129,131,133,135,140/Binding site: calcium (Asp, Asp, Asp, Gln, Glu) #status predict

Query Match 53.3%; Score 388.5; DB 1; Length 148;
Best Local Similarity 52.0%; Pred. No. 1.4e-20;
Matches 77; Conservative 30; Mismatches 38; Indels 3; Gaps 2;

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Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:|||
Db       1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGD 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | ||||  ||| :     |::: ||| ||:|||| |:  |||  |  ||: |  ||
Db      61 GTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGDGFISAAELRHVMTNLGEKLTDEE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARMLAQE 146
           :| ||||||:| ||:|||||| :|:  :
Db     121 VDEMIREADIDGDGQVNYEEFVKMMTSK 148
```

RESULT 2
MCZQF
calmodulin - malaria parasite (Plasmodium falciparum)
N;Alternate names: modulator protein; phosphodiesterase activator; phosphorylase kina
C;Species: Plasmodium falciparum
C;Date: 22-Apr-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
C;Accession: B45594; A49774; S21813
R;Robson, K.J.; Jennings, M.W.

Mol. Biochem. Parasitol. 46, 19-34, 1991
A;Title: The structure of the calmodulin gene of Plasmodium falciparum.
A;Reference number: A45594; MUID:91304518; PMID:1852174
A;Accession: B45594
A;Molecule type: DNA
A;Residues: 1-149 <ROB>
A;Cross-references: GB:M59770; NID:g160127; PIDN:AAA29510.1; PID:g160128
A;Note: sequence extracted from NCBI backbone (NCBIN:42930, NCBIP:42935)
R;Cowman, A.F.; Galatis, D.
Exp. Parasitol. 73, 269-275, 1991
A;Title: Plasmodium falciparum: the calmodulin gene is not amplified or overexpressed in
A;Reference number: A49774; MUID:92008475; PMID:1915742
A;Accession: A49774
A;Molecule type: DNA
A;Residues: 1-149 <COW>
A;Cross-references: EMBL:X56950
C;Genetics:
A;Map position: 14
A;Introns: 27/1
A;Note: only one gene for calmodulin was found
C;Function:
A;Description: calcium-dependent regulation of a number of essential enzymes
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: acetylated amino end; calcium binding; duplication; EF hand; methylated amin
F;2-149/Product: calmodulin #status predicted <MAT>
F;8-40/Domain: calmodulin repeat homology <EF1>
F;44-76/Domain: calmodulin repeat homology <EF2>
F;81-113/Domain: calmodulin repeat homology <EF3>
F;117-149/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F;21,23,25,27,32/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status predicted
F;57,59,61,63,68/Binding site: calcium (Asp, Asp, Asn, Thr, Glu) #status predicted
F;94,96,98,100,105/Binding site: calcium (Asp, Asp, Asp, Tyr, Glu) #status predicted
F;116/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;130,132,134,136,141/Binding site: calcium (Asp, Asp, Asp, Gln, Glu) #status predicted

```
  Query Match             53.3%;  Score 388.5;  DB 1;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 1.4e-20;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: :::|:|||  | ||:|||  :|||  ::: |:| :|||:|: :|:|:|:|| 
Db       1 MADKLTEEQISEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEIDTDG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |:|  ||| ||:||||:|: ||||  |  ||: |  |
Db      61 NGTIDFPEFLTLMARKLKDTDTEEELIEAFRVFDRDGDGYISADELRHVMTNLGEKLTNE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||::||||| :|:
Db     121 EVDEMIREADIDGDGQINYEEFVKMM 146
```

RESULT 3
MCSW
calmodulin - scallop (Patinopecten sp.) (tentative sequence)
N;Alternate names: modulator protein
C;Species: Patinopecten sp.
C;Date: 19-Feb-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A03023
R;Toda, H.; Yazawa, M.; Kondo, K.; Honma, T.; Narita, K.; Yagi, K.
J. Biochem. 90, 1493-1505, 1981
A;Title: Amino acid sequence of calmodulin from scallop (Patinopecten) adductor muscle.
A;Reference number: A91962; MUID:82167261; PMID:7338518
A;Accession: A03023
A;Molecule type: protein
A;Residues: 1-148 <TOD>
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: acetylated amino end; calcium binding; duplication; EF hand; methylated amin
F;7-39/Domain: calmodulin repeat homology <EF1>
F;43-75/Domain: calmodulin repeat homology <EF2>
F;80-112/Domain: calmodulin repeat homology <EF3>
F;116-148/Domain: calmodulin repeat homology <EF4>
F;1/Modified site: acetylated amino end (Ala) #status experimental
F;20,22,24,26,31/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status predicted
F;56,58,60,62,67/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status predicted
F;93,95,97,99,104/Binding site: calcium (Asp, Asp, Asp, Phe, Glu) #status predicted
F;115/Modified site: N6,N6,N6-trimethyllysine (Lys) #status experimental
F;129,131,133,135,140/Binding site: calcium (Asp, Asp, Asp, Gln, Glu) #status predict

```
  Query Match             52.9%;  Score 385.5;  DB 1;  Length 148;
  Best Local Similarity   52.0%;  Pred. No. 2.3e-20;
  Matches   77;  Conservative   29;  Mismatches   39;  Indels    3;  Gaps    2;

Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :|||:|: :|:|||:|||
Db       1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGD 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | ||||  ||| :     |::: ||| ||:|||| |:  |||  |  ||: |  ||
Db      61 GTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGDGFISAAELRHVMTNLGEKLTDEE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARMLAQE 146
           :| ||||||:| ||:||||||  |:  :
Db     121 VDEMIREADIDGDGQVNYEEFVTMMTSK 148
```

RESULT 4
MCHU
calmodulin [validated] - human
N;Alternate names: modulator protein; phosphodiesterase activator; phosphorylase kina
C;Species: Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 30-Jun-1992 #text_change 15-Sep-2000
C;Accession: S48728; S13159; A31787; A28479; A90460; JN0365; I52348; A03021
R;Rhyner, J.A.; Ottiger, M.; Wicki, R.; Greenwood, T.M.; Strehler, E.E.
Eur. J. Biochem. 225, 71-82, 1994
A;Title: Structure of the human CALM1 calmodulin gene and identification of two CALM1
A;Reference number: S48728; MUID:95010144; PMID:7925473
A;Accession: S48728
A;Molecule type: DNA
A;Residues: 1-149 <RHY>
A;Cross-references: EMBL:U11886; NID:g531824; EMBL:U12022; NID:g531825; PIDN:AAB60644
A;Genetics: CAL1
R;Koller, M.; Schnyder, B.; Strehler, E.E.
Biochim. Biophys. Acta 1087, 180-189, 1990
A;Title: Structural organization of the human CaMIII calmodulin gene.
A;Reference number: S13159; MUID:91027929; PMID:2223880
A;Accession: S13159
A;Molecule type: DNA
A;Residues: 1-149 <KOL>
A;Cross-references: EMBL:X52606; EMBL:X52607; EMBL:X52608; NID:g29637; PIDN:CAA36839.
A;Genetics: CAL3
R;Fischer, R.; Koller, M.; Flura, M.; Mathews, S.; Strehler-Page, M.A.; Krebs, J.; Pe
J. Biol. Chem. 263, 17055-17062, 1988
A;Title: Multiple divergent mRNAs code for a single human calmodulin.
A;Reference number: A31787; MUID:89034207; PMID:3182832
A;Accession: A31787
A;Molecule type: mRNA
A;Residues: 1-149 <FIS>
A;Cross-references: GB:J04046; NID:g179887; PIDN:AAA51918.1; PID:g179888
A;Genetics: CAL1
R;SenGupta, B.; Friedberg, F.; Detera-Wadleigh, S.D.
J. Biol. Chem. 262, 16663-16670, 1987
A;Title: Molecular analysis of human and rat calmodulin complementary DNA clones. Evi
A;Reference number: A92620; MUID:88059053; PMID:2445749
A;Accession: A28479
A;Molecule type: mRNA
A;Residues: 1-149 <SEN>
A;Cross-references: GB:J03468; GB:M19311; NID:g179883; PIDN:AAA35641.1; PID:g179884
A;Genetics: CAL2
R;Sasagawa, T.; Ericsson, L.H.; Walsh, K.A.; Schreiber, W.E.; Fischer, E.H.; Titani,
Biochemistry 21, 2565-2569, 1982
A;Title: Complete amino acid sequence of human brain calmodulin.
A;Reference number: A90460; MUID:82231946; PMID:7093203
A;Accession: A90460
A;Molecule type: protein

```
A;Residues: 2-149 <SAS>
R;Alakhov, V.U.; Severin, E.S.; Vinokurov, L.M.; Dudkin, S.M.
Bioorg. Khim. 9, 123-126, 1983
A;Title: Primary structrue of calmodulin from human brain.
A;Reference number: JN0365; MUID:85022799; PMID:6679753
A;Accession: JN0365
A;Molecule type: protein
A;Residues: 2-60,'D',62-104,'Q',106-149 <ALA>
A;Experimental source: brain
R;Wawrzynczak, E.J.; Perham, R.N.
Biochem. Int. 9, 177-185, 1984
A;Title: Isolation and nucleotide sequence of a cDNA encoding human calmodulin.
A;Reference number: I52348; MUID:85022688; PMID:6385987
A;Accession: I52348
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-149 <RES>
A;Cross-references: GB:M27319; NID:g179809; PIDN:AAA35635.1; PID:g179810
R;Chattopadhyaya, R.; Meador, W.E.; Means, A.R.; Quiocho, F.A.
J. Mol. Biol. 228, 1177-1192, 1992
A;Title: Calmodulin structure refined at 1.7 angstrom resolution.
A;Reference number: A57450; MUID:93116061; PMID:1474585
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 5-148
R;Chattopadhyaya, R.; Quiocho, F.A.
submitted to the Brookhaven Protein Data Bank, September 1992
A;Reference number: A51098; PDB:1CLL
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 5-148
R;Ikura, M.; Clore, G.M.; Gronenborn, A.M.; Zhu, G.; Klee, C.B.; Bax, A.
Science 256, 632-638, 1992
A;Title: Solution structure of a calmodulin-target peptide complex by multidimensional N
A;Reference number: A57451; MUID:92263094; PMID:1585175
A;Contents: annotation; conformation of calmodulin and target peptide by (1)H-NMR
R;Meador, W.E.; Means, A.R.; Quiocho, F.A.
Science 257, 1251-1255, 1992
A;Title: Target enzyme recognition by calmodulin: 2.4 angstrom structure of a calmodulin
A;Reference number: A57452; MUID:92390716; PMID:1519061
A;Contents: annotation; X-ray crystallography, 2.4 angstroms, calmodulin and target pept
C;Genetics: <CAL1>
A;Gene: GDB:CALM1; CALML2
A;Cross-references: GDB:127560; OMIM:114180
A;Map position: 14q32-14q32
A;Introns: 1/3; 12/1; 60/1; 95/3; 141/1
A;Note: the multiple calmodulin genes produce different mRNA's but identical protein seq
C;Genetics: <CAL2>
A;Gene: GDB:CALM2; CAMII; PHKD
A;Cross-references: GDB:127561; OMIM:114182
A;Map position: 2p21-2p21
C;Genetics: <CAL3>
A;Gene: GDB:CALM3; PHKD
A;Cross-references: GDB:127562; OMIM:114183
A;Map position: 19q13.3-19q13.3
A;Introns: 1/3; 12/1; 60/1; 95/3; 141/1
C;Complex: in phosphorylase kinase participates in a polymer of 16 chains, four each of
rystalline form is monomeric
C;Function:
A;Description: this protein has multiple, calcium-dependent, regulatory activities in va
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: acetylated amino end; calcium binding; duplication; EF hand; methylated amin
F;2-149/Product: calmodulin #status experimental <MAT>
F;8-40/Domain: calmodulin repeat homology <EF1>
F;44-76/Domain: calmodulin repeat homology <EF2>
F;81-113/Domain: calmodulin repeat homology <EF3>
F;117-149/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F;21,23,25,27,32/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status experimental
F;57,59,61,63,68/Binding site: calcium (Asp, Asp, Asn, Thr, Glu) #status experimental
F;94,96,98,100,105/Binding site: calcium (Asp, Asp, Asn, Tyr, Glu) #status experimental
F;116/Modified site: N6,N6,N6-trimethyllysine (Lys) #status experimental
F;130,132,134,136,141/Binding site: calcium (Asp, Asp, Asp, Gln, Glu) #status experiment

  Query Match            52.7%;  Score 384.5;  DB 1;  Length 149;
  Best Local Similarity  52.1%;  Pred. No. 2.7e-20;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 5
MCRT
calmodulin [validated] - rat
N;Alternate names: modulator protein; phosphodiesterase activator; phosphorylase kina
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Sep-2000
C;Accession: S03206; A30899; S05228; S05227; I57616; B28479; A29082; S17536; A03021
R;Nojima, H.; Sokabe, H.
J. Mol. Biol. 193, 439-445, 1987
A;Title: Structure of a gene for rat calmodulin.
A;Reference number: S03206; MUID:87226204; PMID:3035194
A;Accession: S03206
A;Molecule type: DNA
A;Residues: 1-149 <NO1>
A;Cross-references: EMBL:X13931; NID:g55860; PIDN:CAA32119.1; PID:g1334203
A;Experimental source: strain Wistar-Kyoto
A;Genetics: CAM1
A;Accession: A30899
A;Molecule type: mRNA
A;Residues: 1-149 <NO2>
A;Cross-references: EMBL:X13933; NID:g57040; PIDN:CAA32120.1; PID:g57041
A;Experimental source: strain Sprague-Dawley
R;Nojima, H.
J. Mol. Biol. 208, 269-282, 1989
A;Title: Structural organization of multiple rat calmodulin genes.
A;Reference number: S05227; MUID:89362474; PMID:2527998
A;Accession: S05228
A;Molecule type: DNA
A;Residues: 1-149 <NO4>
A;Cross-references: EMBL:X14265; NID:g55866; PIDN:CAA32478.1; PID:g55867
A;Genetics: CAM2
A;Accession: S05227
A;Molecule type: DNA
A;Residues: 1-149 <NO5>
A;Cross-references: EMBL:X13833; NID:g55863; PIDN:CAA32062.1; PID:g818020
A;Genetics: CAM3
R;Nojima, H.; Kishi, K.; Sokabe, H.
Mol. Cell. Biol. 7, 1873-1880, 1987
A;Title: Multiple calmodulin mRNA species are derived from two distinct genes.
A;Reference number: I57616; MUID:87257889; PMID:3037336
A;Accession: I57616
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-149 <NO3>
A;Cross-references: GB:M17069; NID:g203257; PIDN:AAA40863.1; PID:g203258
R;SenGupta, B.; Friedberg, F.; Detera-Wadleigh, S.D.
J. Biol. Chem. 262, 16663-16670, 1987
A;Title: Molecular analysis of human and rat calmodulin complementary DNA clones. Evi
A;Reference number: A92620; MUID:88059053; PMID:2445749
A;Accession: B28479
A;Molecule type: mRNA
A;Residues: 1-149 <SEN>
A;Cross-references: GB:M19312; NID:g203255; PIDN:AAA40862.1; PID:g203256
R;Sherbany, A.A.; Parent, A.S.; Brosius, J.
DNA 6, 267-272, 1987
A;Title: Rat calmodulin cDNA.
A;Reference number: A29082; MUID:87246077; PMID:2885164
A;Accession: A29082
A;Molecule type: mRNA
```

```
A;Residues: 1-149 <SHE>
A;Cross-references: GB:M16659; NID:g203259; PIDN:AAA40864.1; PID:g203260
R;Wright, L.S.; Collins, J.H.; Finn, K.A.; Siegel, F.L.
Biochim. Biophys. Acta 1079, 174-181, 1991
A;Title: A calmodulin endoproteinase from mitochondrial membranes.
A;Reference number: S17536; MUID:92002131; PMID:1911840
A;Accession: S17536
A;Molecule type: protein
A;Residues: 77-92,94-96 <WRI>
R;Dedman, J.R.; Jackson, R.L.; Schreiber, W.E.; Means, A.R.
J. Biol. Chem. 253, 343-346, 1978
A;Title: Sequence homology of the Ca2+-dependent regulator of cyclic nucleotide phosphod
A;Reference number: A92228; MUID:78066877; PMID:201628
A;Contents: annotation; partial sequence determination
R;Babu, Y.S.; Bugg, C.E.; Cook, W.J.
submitted to the Brookhaven Protein Data Bank, May 1988
A;Reference number: A50576; PDB:3CLN
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 6-129,'N',131-148
R;Babu, Y.S.; Bugg, C.E.; Cook, W.J.
J. Mol. Biol. 204, 191-204, 1988
A;Title: Structure of calmodulin refined at 2.2 A resolution.
A;Reference number: A37299; MUID:89110997; PMID:3145979
A;Contents: annotation; X-ray crystallography, 2.2 angstroms
A;Note: crystals of both rat and cow calmodulin, having identical sequences, were used i
R;Babu, Y.S.; Sack, J.S.; Greenhough, T.J.; Bugg, C.E.; Means, A.R.; Cook, W.J.
Nature 315, 37-40, 1985
A;Title: Three-dimensional structure of calmodulin.
A;Reference number: A37298; MUID:85188323; PMID:3990807
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
C;Comment: Calmodulin regulates many calcium-dependent activities in various tissues.
C;Genetics: <CAM1>
A;Gene: CaMI
A;Introns: 1/3; 12/1; 60/1; 95/3; 141/1
C;Genetics: <CAM2>
A;Gene: CaMII
A;Introns: 1/3; 12/1; 95/3; 141/1
C;Genetics: <CAM3>
A;Gene: CaMIII
A;Introns: 1/3; 12/1; 60/1; 95/3; 141/1
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: acetylated amino end; calcium binding; duplication; EF hand; methylated amin
F;2-149/Product: calmodulin #status experimental <MAT>
F;8-40/Domain: calmodulin repeat homology <EF1>
F;44-76/Domain: calmodulin repeat homology <EF2>
F;81-113/Domain: calmodulin repeat homology <EF3>
F;117-149/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F;21,23,25,27,32/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status experimental
F;57,59,61,63,68/Binding site: calcium (Asp, Asp, Asn, Thr, Glu) #status experimental
F;94,96,98,100,105/Binding site: calcium (Asp, Asp, Asn, Tyr, Glu) #status experimental
F;116/Modified site: N6,N6,N6-trimethyllysine (Lys) #status experimental
F;130,132,134,136,141/Binding site: calcium (Asp, Asp, Asp, Gln, Glu) #status experiment

  Query Match             52.7%;  Score 384.5;  DB 1;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 2.7e-20;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 6
MCCH
calmodulin - chicken
N;Alternate names: modulator protein; phosphodiesterase activator; phosphorylase kina
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999
C;Accession: A92394; I50184; A03021
R;Putkey, J.A.; Ts'ui, K.F.; Tanaka, T.; Lagace, L.; Stein, J.P.; Lai, E.C.; Means, A
J. Biol. Chem. 258, 11864-11870, 1983
A;Title: Chicken calmodulin genes. A species comparison of cDNA sequences and isolati
A;Reference number: A92394; MUID:84008199; PMID:6137485
A;Accession: A92394
A;Molecule type: mRNA
A;Residues: 1-149 <PUT>
A;Cross-references: GB:L00101; EMBL:K00430; NID:g211396; PIDN:AAA48653.1; PID:g211398
R;Simmen, R.C.M.; Tanaka, T.; Ts'ui, K.F.; Putkey, J.A.; Scott, M.J.; Lai, E.C.; Mean
J. Biol. Chem. 260, 907-912, 1985
A;Title: The structural organization of the chicken calmodulin gene.
A;Reference number: A37301; MUID:85104969; PMID:2981850
A;Contents: annotation
R;Simmen, R.C.M.; Tanaka, T.; Ts'ui, K.F.; Putkey, J.A.; Scott, M.J.; Lai, E.C.; Mean
J. Biol. Chem. 262, 4928-4929, 1987
A;Title: The structural organization of the chicken calmodulin gene: a correction.
A;Reference number: A37302
A;Contents: annotation
R;Iida, Y.
Bull. Chem. Soc. Jpn. 57, 2667-2668, 1984
A;Title: cDNA sequences and molecular evolution of calmodulin genes of chicken and ee
A;Reference number: I50184
A;Accession: I50184
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-149 <IID>
A;Cross-references: GB:M36167; NID:g211385; PIDN:AAA48650.1; PID:g211386
C;Comment: This protein has multiple, calcium-dependent, regulatory activities in var
C;Genetics:
A;Introns: 1/3; 12/1; 60/1; 95/3; 141/1
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; duplication; EF hand; methylated amino acid
F;2-149/Product: calmodulin #status predicted <MAT>
F;8-40/Domain: calmodulin repeat homology <EF1>
F;44-76/Domain: calmodulin repeat homology <EF2>
F;81-113/Domain: calmodulin repeat homology <EF3>
F;117-149/Domain: calmodulin repeat homology <EF4>
F;21,23,25,27,32/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status predicted
F;57,59,61,63,68/Binding site: calcium (Asp, Asp, Asn, Thr, Glu) #status predicted
F;94,96,98,100,105/Binding site: calcium (Asp, Asp, Asn, Tyr, Glu) #status predicted
F;116/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;130,132,134,136,141/Binding site: calcium (Asp, Asp, Asp, Gln, Glu) #status predict

  Query Match             52.7%;  Score 384.5;  DB 1;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 2.7e-20;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 7
I51202
calmodulin - duck
N;Alternate names: modulator protein; phosphodiesterase activator; phosphorylase kina
C;Species: Anas platyrhynchos (domestic duck)
C;Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 22-Jun-1999
C;Accession: I51202
R;Kimura, N.; Kurosawa, N.; Kondo, K.; Tsukada, Y.
Brain Res. Mol. Brain Res. 17, 351-355, 1993
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A;Title: Molecular cloning of the kainate-binding protein and calmodulin genes which are
A;Reference number: I51201; MUID:93287810; PMID:8389959
A;Accession: I51202
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <KIM>
A;Cross-references: GB:D83350; NID:g1199918; PIDN:BAA11896.1; PID:g1199919
C;Comment: This protein has multiple, calcium-dependent, regulatory activities in variou
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; duplication; EF hand; methylated amino acid
F;2-149/Product: calmodulin #status predicted <MAT>
F;8-40/Domain: calmodulin repeat homology <EF1>
F;44-76/Domain: calmodulin repeat homology <EF2>
F;81-113/Domain: calmodulin repeat homology <EF3>
F;117-149/Domain: calmodulin repeat homology <EF4>
F;116/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted

  Query Match            52.7%;  Score 384.5;  DB 1;  Length 149;
  Best Local Similarity  52.1%;  Pred. No. 2.7e-20;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 8
JC1305
calmodulin - Japanese medaka
C;Species: Oryzias latipes (Japanese medaka)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: JC1305
R;Matsuo, K.; Sato, K.; Ikeshima, H.; Shimoda, K.; Takano, T.
Gene 119, 279-281, 1992
A;Title: Four synonymous genes encode calmodulin in the teleost fish, medaka (Oryzias la
A;Reference number: JC1305; MUID:93012998; PMID:1398109
A;Accession: JC1305
A;Molecule type: mRNA
A;Residues: 1-149 <MAT>
A;Cross-references: DDBJ:D10363
C;Genetics:
A;Gene: CamI
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; duplication; EF hand
F;8-40/Domain: calmodulin repeat homology <EF1>
F;44-76/Domain: calmodulin repeat homology <EF2>
F;81-113/Domain: calmodulin repeat homology <EF3>

  Query Match            52.7%;  Score 384.5;  DB 2;  Length 149;
  Best Local Similarity  52.1%;  Pred. No. 2.7e-20;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 9
I51402
calmodulin - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C;Accession: I51402; I51403
R;Chien, Y.
Mol. Cell. Biol. 4, 507-513, 1984
A;Title: Isolation and characterization of calmodulin genes from Xenopus laevis.
A;Reference number: I51402; MUID:84191128; PMID:6325880
A;Accession: I51402
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-149 <CHI>
A;Cross-references: GB:K01944; NID:g214016; PIDN:AAA49668.1; PID:g214017
A;Note: clone 11G2
A;Accession: I51403
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-149 <CH2>
A;Cross-references: GB:K01945; NID:g214018; PIDN:AAA49669.1; PID:g214019
A;Note: clone 71
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: EF hand
F;8-40/Domain: calmodulin repeat homology <EF1>
F;44-76/Domain: calmodulin repeat homology <EF2>
F;81-113/Domain: calmodulin repeat homology <EF3>
F;117-149/Domain: calmodulin repeat homology <EF4>

  Query Match            52.7%;  Score 384.5;  DB 2;  Length 149;
  Best Local Similarity  52.1%;  Pred. No. 2.7e-20;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 10
S37707
calmodulin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Dec-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999
C;Accession: S37707; I49566; I49569
R;Kato, K.
J. Neurosci. 2, 704-711, 1991
A;Title: A collection of cDNA clones with specific expression patterns in mouse brain
A;Reference number: S37707
A;Accession: S37707
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-149 <KAT>
A;Cross-references: EMBL:X61432; NID:g50273; PIDN:CAA43674.1; PID:g50274
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
R;Bender, P.K.; Dedman, J.R.; Emerson, C.P.
J. Biol. Chem. 263, 9733-9737, 1988
A;Title: The abundance of calmodulin mRNAs is regulated in phosphorylase kinase-defic
A;Reference number: I49566; MUID:88257100; PMID:3384819
A;Accession: I49566
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-149 <RES>
A;Cross-references: GB:M19380; NID:g469419; PIDN:AAA66181.1; PID:g469420
A;Experimental source: skeletal muscle
R;Danchin, A.; Sezer, O.; Glaser, P.; Chalon, P.; Caput, D.
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Gene 80, 145-149, 1989
A;Title: cloning and expression of mouse-brain calmodulin as an activator of bordetella
A;Reference number: I49569; MUID:90006775; PMID:2551780
A;Accession: I49569
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-149 <RE2>
A;Cross-references: GB:M27844; NID:g192364; PIDN:AAA37365.1; PID:g192365
C;Genetics:
A;Gene: Cam III; CaM
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: EF hand
F;8-40/Domain: calmodulin repeat homology <EF1>
F;44-76/Domain: calmodulin repeat homology <EF2>

  Query Match             52.7%;  Score 384.5;  DB 2;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 2.7e-20;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :|||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 11
MCJZR
calmodulin - sea pansy (Renilla reniformis) (tentative sequence)
N;Alternate names: modulator protein
C;Species: Renilla reniformis (sea pansy)
C;Date: 31-Dec-1991 #sequence_revision 30-Jun-1992 #text_change 24-Nov-1999
C;Accession: A90036; A03023
R;Jamieson Jr., G.A.; Bronson, D.D.; Schachat, F.H.; Vanaman, T.C.
Ann. N. Y. Acad. Sci. 356, 1-13, 1980
A;Title: Structure and function relationships among calmodulins and troponin C-like prot
A;Reference number: A90036; MUID:81205529; PMID:6263143
A;Accession: A90036
A;Molecule type: protein
A;Residues: 1-147 <JAM>
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; methylated amino a
F;6-38/Domain: calmodulin repeat homology <EF1>
F;42-74/Domain: calmodulin repeat homology <EF2>
F;79-111/Domain: calmodulin repeat homology <EF3>
F;115-147/Domain: calmodulin repeat homology <EF4>
F;1/Modified site: blocked amino end (Ala) #status experimental
F;19,21,23,25,30/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status predicted
F;55,57,59,61,66/Binding site: calcium (Asp, Asp, Asx, Thr, Glu) #status predicted
F;92,94,96,98,103/Binding site: calcium (Asp, Asp, Asp, Phe, Glu) #status predicted
F;114/Modified site: N6,N6,N6-trimethyllysine (Lys) #status experimental
F;128,130,132,134,139/Binding site: calcium (Asp, Asp, Asp, Gln, Glu) #status predicted

  Query Match             52.6%;  Score 383.5;  DB 1;  Length 147;
  Best Local Similarity   51.4%;  Pred. No. 3.2e-20;
  Matches   75;  Conservative   31;  Mismatches   37;  Indels    3;  Gaps    2;

Qy       4 ELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGDGE 63
           :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :|||:|: :|:|||:||:|
Db       2 DLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGBGT 61

Qy      64 ISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120
           | | ||||  ||| :     |::: ||| ||:|||| |:  |||  |  ||: |  ||:|
Db      62 IDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGDGFISAAELRHVMTNLGEKLTDEEVD 121

Qy     121 AMIREADVDQDGRVNYEEFARMLAQE 146
           ||||||:| ||:|||||| :|:  :
Db     122 EMIREADIDGDGQVNYEEFVKMMTSK 147


RESULT 12
MCEE
calmodulin - electric eel
N;Alternate names: modulator protein; phosphodiesterase activator; phosphorylase kina
C;Species: Electrophorus electricus (electric eel)
C;Date: 25-Feb-1985 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999
C;Accession: A03022; A60781; I50534
R;Lagace, L.; Chandra, T.; Woo, S.L.C.; Means, A.R.
J. Biol. Chem. 258, 1684-1688, 1983
A;Title: Identification of multiple species of calmodulin messenger RNA using a full
A;Reference number: A03022; MUID:83108962; PMID:6185488
A;Accession: A03022
A;Molecule type: mRNA
A;Residues: 1-149 <LAG>
A;Cross-references: GB:J00931; NID:g213131
A;Experimental source: electroplax
A;Note: this ORF is not annotated in GenBank entry ELCCALMA, release 103
R;Toda, H.; Abe, Y.; Yazawa, M.; Yagi, K.
Seikagaku 57, 1037, 1985
A;Title: Amino acid sequence of sea cucumber calmodulin.
A;Reference number: JK0011
A;Note: author-supplied citation
A;Accession: A60781
A;Molecule type: protein
A;Residues: 2-74,'R',76-149 <YAZ>
A;Note: 75-Lys also found
R;Iida, Y.
Bull. Chem. Soc. Jpn. 57, 2667-2668, 1984
A;Title: cDNA sequences and molecular evolution of calmodulin genes of chicken and ee
A;Reference number: I50184
A;Accession: I50534
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-149 <IID>
A;Cross-references: GB:M36168; NID:g213129; PIDN:AAA49236.1; PID:g213130
C;Comment: This protein has multiple, calcium-dependent, regulatory activities in var
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; duplication; EF hand; methylated amino acid
F;2-149/Product: calmodulin #status predicted <MAT>
F;8-40/Domain: calmodulin repeat homology <EF1>
F;44-76/Domain: calmodulin repeat homology <EF2>
F;81-113/Domain: calmodulin repeat homology <EF3>
F;117-149/Domain: calmodulin repeat homology <EF4>
F;21,23,25,27,32/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status predicted
F;57,59,61,63,68/Binding site: calcium (Asp, Asp, Asn, Thr, Glu) #status predicted
F;94,96,98,100,105/Binding site: calcium (Asp, Asp, Asn, Tyr, Glu) #status predicted
F;116/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;130,132,134,136,141/Binding site: calcium (Asp, Asp, Asp, Gln, Glu) #status predict

  Query Match             52.5%;  Score 382.5;  DB 1;  Length 149;
  Best Local Similarity   50.7%;  Pred. No. 3.8e-20;
  Matches   74;  Conservative   31;  Mismatches   38;  Indels    3;  Gaps    1;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :|||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLTAARKARAGL---EDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||   |         |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMAKKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 13
MCAZS
calmodulin - sea squirt
N;Alternate names: modulator protein
```

C;Species: Ascidiacea indet. (sea squirt)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 17-Apr-1998
C;Accession: JK0015
R;Yazawa, M.; Toda, H.; Sakiyama, F.; Yagi, K.
submitted to JIPID, May 1988
A;Reference number: A94540
A;Accession: JK0015
A;Molecule type: protein
A;Residues: 1-148 <YAZ>
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: acetylated amino end; calcium binding; duplication; EF hand; methylated amin
F;7-39/Domain: calmodulin repeat homology <EF1>
F;43-75/Domain: calmodulin repeat homology <EF2>
F;80-112/Domain: calmodulin repeat homology <EF3>
F;116-148/Domain: calmodulin repeat homology <EF4>
F;1/Modified site: acetylated amino end (Ala) #status experimental
F;20,22,24,26,31/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status predicted
F;56,58,60,62,67/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status predicted
F;93,95,97,99,104/Binding site: calcium (Asp, Asp, Asn, Phe, Glu) #status predicted
F;115/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;129,131,133,135,140/Binding site: calcium (Asp, Asp, Asp, Gln, Glu) #status predicted

Query Match 52.2%; Score 380.5; DB 1; Length 148;
Best Local Similarity 51.4%; Pred. No. 5.2e-20;
Matches 76; Conservative 30; Mismatches 39; Indels 3; Gaps 2;

```
Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:|||
Db       1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGD 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | ||||  ||| :    |::: ||| ||:||:| |:  ||| |  ||: |  ||
Db      61 GTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDEE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARMLAQE 146
           :| ||||||:| ||:||||||  |:  :
Db     121 VDEMIREADIDGDGQVNYEEFVTMMTSK 148
```

RESULT 14
MCFF
calmodulin [validated] - fruit fly (Drosophila melanogaster)
N;Alternate names: modulator protein; phosphodiesterase activator; phosphorylase kinase
C;Species: Drosophila melanogaster
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Sep-2000
C;Accession: S01173; A27515; S10637
R;Smith, V.L.; Doyle, K.E.; Maune, J.F.; Munjaal, R.P.; Beckingham, K.
J. Mol. Biol. 196, 471-485, 1987
A;Title: Structure and sequence of the Drosophila melanogaster calmodulin gene.
A;Reference number: S01173; MUID:88062687; PMID:3119855
A;Accession: S01173
A;Molecule type: DNA
A;Residues: 1-149 <SMI>
A;Cross-references: EMBL:X05948
R;Yamanaka, M.K.; Saugstad, J.A.; Hanson-Painton, O.; McCarthy, B.J.; Tobin, S.L.
Nucleic Acids Res. 15, 3335-3348, 1987
A;Title: Structure and expression of the Drosophila calmodulin gene.
A;Reference number: A27515; MUID:87203365; PMID:3106931
A;Accession: A27515
A;Molecule type: DNA; mRNA
A;Residues: 2-149 <YAM>
A;Cross-references: EMBL:Y00133; NID:g7687; PIDN:CAA68327.1; PID:g7688
R;Goerlach, M.; Dieter, P.; Seydewitz, H.H.; Kaiser, C.; Witt, I.; Marme, D.
Biochim. Biophys. Acta 832, 228-232, 1985
A;Title: Characterisation of calmodulin from Drosophila heads.
A;Reference number: A30897
A;Contents: annotation
A;Note: trimethyllysine is absent from fruit fly calmodulin
R;Taylor, D.A.; Sack, J.S.; Maune, J.F.; Beckingham, K.; Quiocho, F.A.
J. Biol. Chem. 266, 21375-21380, 1991
A;Title: Structure of a recombinant calmodulin from Drosophila melanogaster refined at 2
A;Reference number: A58243; MUID:92042027; PMID:1939171
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 2-148
A;Note: recombinant form expressed in Escherichia coli
R;Taylor, D.A.; Sack, J.S.; Maune, J.F.; Beckingham, K.; Quiocho, F.A.
submitted to the Brookhaven Protein Data Bank, June 1991
A;Reference number: A50648; PDB:4CLN
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 2-148
C;Genetics:
A;Gene: Cal49A
A;Cross-references: FlyBase:FBgn0000253
A;Map position: 2-[64]
A;Introns: 1/3; 60/1; 141/1
C;Function:
A;Description: this protein has multiple, calcium-dependent, regulatory activities in
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; duplication; EF hand
F;2-149/Product: calmodulin #status predicted <MAT>
F;8-40/Domain: calmodulin repeat homology <EF1>
F;44-76/Domain: calmodulin repeat homology <EF2>
F;81-113/Domain: calmodulin repeat homology <EF3>
F;117-149/Domain: calmodulin repeat homology <EF4>
F;21,23,25,27,32/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status experimental
F;57,59,61,63,68/Binding site: calcium (Asp, Asp, Asn, Thr, Glu) #status experimental
F;94,96,98,100,105/Binding site: calcium (Asp, Asp, Asn, Phe, Glu) #status experiment
F;116/Modified site: N6,N6,N6-trimethyllysine (Lys) #status absent
F;130,132,134,136,141/Binding site: calcium (Asp, Asp, Asp, Gln, Glu) #status experim

Query Match 52.2%; Score 380.5; DB 1; Length 149;
Best Local Similarity 51.0%; Pred. No. 5.2e-20;
Matches 76; Conservative 31; Mismatches 39; Indels 3; Gaps 2;

```
Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :    |::: ||| ||:||:| |:  ||| |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARMLAQE 146
           |:| ||||||:| ||:||||||  |:  :
Db     121 EVDEMIREADIDGDGQVNYEEFVTMMTSK 149
```

RESULT 15
MCGAC
calmodulin - California sea hare
N;Alternate names: modulator protein
C;Species: Aplysia californica (California sea hare)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999
C;Accession: S13248; A30898
R;Swanson, M.E.; Sturner, S.F.; Schwartz, J.H.
J. Mol. Biol. 216, 545-553, 1990
A;Title: Structure and expression of the Aplysia californica calmodulin gene.
A;Reference number: S13248; MUID:91080147; PMID:2258931
A;Accession: S13248
A;Molecule type: DNA
A;Residues: 2-149 <SWA>
A;Cross-references: GB:X56888; NID:g5571; PIDN:CAA40207.1; PID:g5572
A;Accession: A30898
A;Molecule type: mRNA
A;Residues: 1-149 <SW2>
A;Cross-references: GB:X56888; NID:g5571; PIDN:CAA40207.1; PID:g5572
C;Genetics:
A;Introns: 1/3; 12/1; 60/1; 141/1
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; duplication; EF hand; methylated amino acid
F;2-149/Product: calmodulin #status predicted <MAT>
F;8-40/Domain: calmodulin repeat homology <EF1>
F;44-76/Domain: calmodulin repeat homology <EF2>
F;81-113/Domain: calmodulin repeat homology <EF3>
F;117-149/Domain: calmodulin repeat homology <EF4>
F;21,23,25,27,32/Binding site: calcium (Asp, Asp, Asp, Thr, Glu) #status predicted
F;57,59,61,63,68/Binding site: calcium (Asp, Asp, Asn, Thr, Glu) #status predicted
F;94,96,98,100,105/Binding site: calcium (Asp, Asp, Asn, Phe, Glu) #status predicted

F;116/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;130,132,134,136,141/Binding site: calcium (Asp, Asp, Asp, Gln, Glu) #status predicted

Query Match 52.2%; Score 380.5; DB 1; Length 149;
Best Local Similarity 51.0%; Pred. No. 5.2e-20;
Matches 76; Conservative 31; Mismatches 39; Indels 3; Gaps 2;

```
Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:| |:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARMLAQE 146
           |:| ||||||:| ||:||||||  |:  :
Db     121 EVDEMIREADIDGDGQVNYEEFVTMMTSK 149
```

Search completed: March 24, 2003, 17:45:37
Job time : 19 secs

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 24, 2003, 17:43:25 ; Search time 12 Seconds
(without alignments)
504.629 Million cell updates/sec

Title: US-10-031-403-1
Perfect score: 729
Sequence: 1 MAGELTPEEEAQYKKAFSAV.....DVDQDGRVNYEEFARMLAQE 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	729	100.0	146	1	CLSP_HUMAN	Q9nztl homo sapien
2	388.5	53.3	148	1	CALM_METSE	P02596 metridium s
3	388.5	53.3	149	1	CALM_PLAFA	P24044 plasmodium
4	385.5	52.9	148	1	CALM_PATSP	P02595 patinopecte
5	380.5	52.2	148	1	CALM_PYUSP	P11121 pyuridae sp
6	379.5	52.1	148	1	CALM_HUMAN	P02593 homo sapien
7	378.5	51.9	148	1	CALM_STIJA	P21251 stichopus j
8	377.5	51.8	148	1	CALM_ELEEL	P02594 electrophor
9	375.5	51.5	148	1	CALM_DROME	P07181 drosophila
10	371	50.9	148	1	CLM4_MOUSE	Q9jm83 mus musculu
11	369.5	50.7	148	1	CALM_PHYIN	P27165 phytophthor
12	369.5	50.7	162	1	CALM_CHLRE	P04352 chlamydomon
13	368.5	50.5	148	1	CALM_BLAEM	Q9hfy6 blastocladi
14	368.5	50.5	148	1	CLM_PLEOS	O94739 pleurotus o
15	367.5	50.4	148	1	CALM_PLECO	P11120 pleurotus c
16	366.5	50.3	148	1	CALM_TRYCR	P18061 trypanosoma
17	365.5	50.1	148	1	CALM_STYLE	P27166 stylonychia
18	365.5	50.1	148	1	CALM_TETPY	P02598 tetrahymena
19	365.5	50.1	148	1	CALM_TRYBB	P04465 trypanosoma
20	364.5	50.0	148	1	CALM_EUGGR	P11118 euglena gra
21	364.5	50.0	155	1	CALF_NAEGR	P53440 naegleria g
22	362.5	49.7	148	1	CALM_PARTE	P07463 paramecium
23	361.5	49.6	151	1	CALM_DICDI	P02599 dictyosteli
24	360.5	49.5	148	1	CALM_ACHKL	P15094 achlya kleb
25	358.5	49.2	148	1	CALS_CHICK	P02597 gallus gall
26	357.5	49.0	148	1	CALM_SPIOL	P04353 spinacia ol
27	355.5	48.8	138	1	CALL_ARBPU	P05932 arbacia pun
28	354.5	48.6	148	1	CALM_LYCES	P27161 lycopersico
29	354	48.6	149	1	CALM_WHEAT	P04464 triticum ae
30	353.5	48.5	148	1	CALM_HORVU	P13565 hordeum vul
31	353.5	48.5	148	1	CALM_MEDSA	P17928 medicago sa
32	353.5	48.5	148	1	CALM_ORYSA	P29612 oryza sativ
33	352.5	48.4	148	1	CALL_HUMAN	P27482 homo sapien
34	350.5	48.1	148	1	CAL1_PETHY	P27162 petunia hyb
35	350.5	48.1	148	1	CAL6_ARATH	Q03509 arabidopsis
36	350.5	48.1	148	1	CALM_HELAN	P93171 helianthus
37	350.5	48.1	148	1	CALM_MAIZE	P41040 zea mays (m
38	350.5	48.1	148	1	CALM_SOLTU	P13868 solanum tub
39	350.5	48.1	183	1	CAL3_PETHY	P27164 petunia hyb
40	349.5	47.9	148	1	CAL2_PETHY	P27163 petunia hyb
41	347.5	47.7	148	1	CAL2_ARATH	P25069 arabidopsis
42	347.5	47.7	148	1	CALM_CAPAN	P93087 capsicum an
43	344.5	47.3	131	1	CALN_CHICK	P05419 gallus gall
44	342.5	47.0	148	1	CAL4_ARATH	Q03510 arabidopsis
45	340.5	46.7	148	1	CALM_EMENI	P19533 emericella

ALIGNMENTS

RESULT 1
CLSP_HUMAN
ID CLSP_HUMAN STANDARD; PRT; 146 AA.
AC Q9NZT1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calmodulin-like skin protein.
GN CLSP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Skin;
RX MEDLINE=20239936; PubMed=10777582;
RA Mehul B., Bernard D., Simonetti L., Bernard M.A., Schmidt R.;
RT "Identification and cloning of a new calmodulin-like protein from
RT human epidermis.";
RL J. Biol. Chem. 275:12841-12847(2000).
CC -!- FUNCTION: BINDS CALCIUM. MAY BE INVOLVED IN TERMINAL
CC DIFFERENTIATION OF KERATINOCYTES.
CC -!- SUBUNIT: ASSOCIATES WITH TRANSGLUTAMINASE 3.
CC -!- TISSUE SPECIFICITY: PARTICULARLY ABUNDANT IN THE EPIDERMIS WHERE
CC ITS EXPRESSION IS DIRECTLY RELATED TO KERATINOCYTE
CC DIFFERENTIATION. VERY LOW EXPRESSION IN LUNG.
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC ----------

CC ----------
DR EMBL; AF172852; AAF66821.1; -.
DR HSSP; P02593; 1FW4.
DR MIM; 605183; -.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat.
FT CA_BIND 21 32 EF-HAND 1 (POTENTIAL).
FT CA_BIND 57 68 EF-HAND 2 (POTENTIAL).
FT CA_BIND 91 102 EF-HAND 3 (POTENTIAL).
FT CA_BIND 127 138 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 146 AA; 15920 MW; 6F565F8E04B994CC CRC64;

Query Match 100.0%; Score 729; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

April 28, 2000 done.

```
Qy      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60

Qy     61 DGEISFQEFLTAARKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DGEISFQEFLTAARKARAGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120

Qy    121 AMIREADVDQDGRVNYEEFARMLAQE 146
          |||||||||||||||||||||||||
Db    121 AMIREADVDQDGRVNYEEFARMLAQE 146
```

RESULT 2
CALM_METSE
ID CALM_METSE STANDARD; PRT; 148 AA.
AC P02596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calmodulin.
OS Metridium senile (Brown sea anemone) (Frilled sea anemone), and
OS Renilla reniformis (Sea pansy).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Metridiidae; Metridium.
OX NCBI_TaxID=6116, 6136;
RN [1]
RP SEQUENCE.
RX MEDLINE=81062446; PubMed=6108109;
RA Takagi T., Nemoto T., Konishi K., Yazawa M., Yagi K.;
RT "The amino acid sequence of the calmodulin obtained from sea anemone
RT (metridium senile) muscle.";
RL Biochem. Biophys. Res. Commun. 96:377-381(1980).
RN [2]
RP SEQUENCE.
RX MEDLINE=81205529; PubMed=6263143;
RA Jamieson G.A. Jr., Bronson D.D., Schachat F.H., Vanaman T.C.;
RT "Structure and function relationships among calmodulins and troponin
RT C-like proteins from divergent eukaryotic organisms.";
RL Ann. N.Y. Acad. Sci. 356:1-13(1980).
CC -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC   ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC   CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC   PHOSPHATASES.
CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC   SITES.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR PIR; A90223; MCXAM.
DR PIR; A90036; MCJZR.
DR HSSP; P02593; 1AK8.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat; Methylation.
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 115 115 METHYLATION (TRI-).
FT CA_BIND 20 31 EF-HAND 1.
FT CA_BIND 56 67 EF-HAND 2.
FT CA_BIND 93 104 EF-HAND 3.
FT CA_BIND 129 140 EF-HAND 4.
SQ SEQUENCE 148 AA; 16708 MW; 4CEEEBE8C4D750AA CRC64;

```
  Query Match             53.3%;  Score 388.5;  DB 1;  Length 148;
  Best Local Similarity   52.0%;  Pred. No. 7.3e-19;
  Matches   77;  Conservative   30;  Mismatches   38;  Indels    3;  Gaps    2;

Qy      2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
          | :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:|||
Db      1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGD 60

Qy     62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
          | | | |||| ||| :    |::: ||| ||:|||| |:  |||  |  ||: |  ||
Db     61 GTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGDGFISAAELRHVMTNLGEKLTDEE 120

Qy    119 LDAMIREADVDQDGRVNYEEFARMLAQE 146
          :| ||||||:| ||:|||||| :|:  :
Db    121 VDEMIREADIDGDGQVNYEEFVKMMTSK 148
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RESULT 3
CALM_PLAFA
ID CALM_PLAFA STANDARD; PRT; 149 AA.
AC P24044;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Calmodulin.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate FC27;
RX MEDLINE=92008475; PubMed=1915742;
RA Cowman A.F., Galatis D.;
RT "Plasmodium falciparum: the calmodulin gene is not amplified or
RT overexpressed in chloroquine resistant or sensitive isolates.";
RL Exp. Parasitol. 73:269-275(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91304518; PubMed=1852174;
RA Robson K.J.H., Jennings M.W.;
RT "The structure of the calmodulin gene of Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 46:19-34(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93376007; PubMed=8366883;
RA Robson K.J.H.;
RT "Sequence diversity in the intron of the calmodulin gene from
RT Plasmodium falciparum.";
RL Mol. Biochem. Parasitol. 60:1-8(1993).
CC -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC   ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC   CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC   PHOSPHATASES.
CC -!- MISCELLANEOUS: CALMODULIN IS NOT INVOLVED IN THE MECHANISM OF
CC   CHLOROQUINE RESISTANCE.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC --
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC --
DR EMBL; M59349; AAA29509.1; -.
DR EMBL; X56950; CAA40264.1; -.
DR EMBL; M59770; AAA29510.1; -.
DR EMBL; M99442; AAA29508.1; -.
DR PIR; S21813; S21813.
DR PIR; B45594; B45594.
DR PIR; A49774; A49774.
DR HSSP; P02593; 1CDM.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding.
FT CA_BIND 21 32 EF-HAND 1.
FT CA_BIND 57 68 EF-HAND 2.
FT CA_BIND 94 105 EF-HAND 3.

```
FT   CA_BIND     130    141       EF-HAND 4.
FT   CONFLICT     28     30       MISSING (IN REF. 1).
SQ   SEQUENCE   149 AA;  16931 MW;  30D806FDA42BC173 CRC64;

  Query Match             53.3%;  Score 388.5;  DB 1;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 7.3e-19;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: :::|:||| | ||:||| :||| ::: |:| :||:|: :|:|:|:||
Db       1 MADKLTEEQISEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEIDTDG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :     |:| ||| ||:||||:|: |||| |  ||: | |
Db      61 NGTIDFPEFLTLMARKLKDTDTEEELIEAFRVFDRDGDGYISADELRHVMTNLGEKLTNE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||::|||| :|:
Db     121 EVDEMIREADIDGDGQINYEEFVKMM 146


RESULT 4
CALM_PATSP
ID   CALM_PATSP     STANDARD;      PRT;   148 AA.
AC   P02595;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin.
OS   Patinopecten sp. (Scallop).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
OC   Pectinoidea; Pectinidae; Patinopecten.
OX   NCBI_TaxID=6574;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82167261; PubMed=7338518;
RA   Toda H., Yazawa M., Kondo K., Honma T., Narita K., Yagi K.;
RT   "Amino acid sequence of calmodulin from scallop (Patinopecten)
RT   adductor muscle.";
RL   J. Biochem. 90:1493-1505(1981).
CC   -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC       ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC       CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC       PHOSPHATASES.
CC   -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC       SITES.
CC   -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR   PIR; A03023; MCSW.
DR   HSSP; P07181; 4CLN.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium-binding; Repeat; Acetylation.
FT   MOD_RES       1      1       ACETYLATION.
FT   CA_BIND      20     31       EF-HAND 1.
FT   CA_BIND      56     67       EF-HAND 2.
FT   CA_BIND      93    104       EF-HAND 3.
FT   CA_BIND     129    140       EF-HAND 4.
SQ   SEQUENCE   148 AA;  16681 MW;  4CEEEBE8C4C5C0AA CRC64;

  Query Match             52.9%;  Score 385.5;  DB 1;  Length 148;
  Best Local Similarity   52.0%;  Pred. No. 1.1e-18;
  Matches   77;  Conservative   29;  Mismatches   39;  Indels    3;  Gaps    2;

Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:|||
Db       1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGD 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | |||| ||| :     |::: ||| ||:|||| |: ||| | ||: | ||
Db      61 GTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGDGFISAAELRHVMTNLGEKLTDEE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARMLAQE 146
           :| ||||||:| ||:|||||| |:  :
Db     121 VDEMIREADIDGDGQVNYEEFVTMMTSK 148


RESULT 5
CALM_PYUSP
ID   CALM_PYUSP     STANDARD;      PRT;   148 AA.
AC   P11121;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin.
OS   Pyuridae sp. (Sea squirt).
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC   Stolidobranchia; Pyuridae; unclassified Pyuridae.
OX   NCBI_TaxID=7734;
RN   [1]
RP   SEQUENCE.
RA   Yazawa M., Toda H., Sakiyama F., Yagi K.;
RL   Submitted (MAY-1988) to the PIR data bank.
CC   -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC       ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC       CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC       PHOSPHATASES.
CC   -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC       SITES.
CC   -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR   PIR; JK0015; MCAZS.
DR   HSSP; P07181; 4CLN.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium-binding; Repeat; Methylation; Acetylation.
FT   MOD_RES       1      1       ACETYLATION.
FT   MOD_RES     115    115       METHYLATION.
FT   CA_BIND      20     31       EF-HAND 1.
FT   CA_BIND      56     67       EF-HAND 2.
FT   CA_BIND      93    104       EF-HAND 3.
FT   CA_BIND     129    140       EF-HAND 4.
SQ   SEQUENCE   148 AA;  16680 MW;  4CEEEBE57FA87BCA CRC64;

  Query Match             52.2%;  Score 380.5;  DB 1;  Length 148;
  Best Local Similarity   51.4%;  Pred. No. 2.4e-18;
  Matches   76;  Conservative   30;  Mismatches   39;  Indels    3;  Gaps    2;

Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:|||
Db       1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGD 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | |||| ||| :     |::: ||| ||:||:|: |:  ||| | ||: | ||
Db      61 GTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDEE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARMLAQE 146
           :| ||||||:| ||:|||||| |:  :
Db     121 VDEMIREADIDGDGQVNYEEFVTMMTSK 148


RESULT 6
CALM_HUMAN
ID   CALM_HUMAN     STANDARD;      PRT;   148 AA.
AC   P02593; P99014; P70667; Q61379; Q61380;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin.
GN   (CALM1 OR CAM1 OR CALM OR CAM) AND (CALM2 OR CAM2 OR CAMB) AND
GN   (CALM3 OR CAM3 OR CAMC).
OS   Homo sapiens (Human),
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OS Mus musculus (Mouse),
OS Rattus norvegicus (Rat),
OS Oryctolagus cuniculus (Rabbit),
OS Bos taurus (Bovine),
OS Gallus gallus (Chicken),
OS Anas platyrhynchos (Domestic duck),
OS Xenopus laevis (African clawed frog),
OS Arbacia punctulata (Punctuate sea urchin),
OS Oncorhynchus sp. (Salmon), and
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10090, 10116, 9986, 9913, 9031, 8839, 8355, 7641,
OX 8025, 8090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=89034207; PubMed=3182832;
RA Fischer R., Koller M., Flura M., Mathews S., Strehler-Page M.A.,
RA Krebs J., Penniston J.T., Carafoli E., Strehler E.E.;
RT "Multiple divergent mRNAs code for a single human calmodulin.";
RL J. Biol. Chem. 263:17055-17062(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=88059053; PubMed=2445749;
RA Sengupta B., Friedberg F., Detera-Wadleigh S.D.;
RT "Molecular analysis of human and rat calmodulin complementary DNA
RT clones. Evidence for additional active genes in these species.";
RL J. Biol. Chem. 262:16663-16670(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=85022688; PubMed=6385987;
RA Wawrzynczak E.J., Perham R.N.;
RT "Isolation and nucleotide sequence of a cDNA encoding human
RT calmodulin.";
RL Biochem. Int. 9:177-185(1984).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Blood;
RX MEDLINE=95010144; PubMed=7925473;
RA Rhyner J.A., Ottiger M., Wicki R., Greenwood T.M., Strehler E.E.;
RT "Structure of the human CALM1 calmodulin gene and identification of
RT two CALM1-related pseudogenes CALM1P1 and CALM1P2.";
RL Eur. J. Biochem. 225:71-82(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Lymphoma;
RA Kato S.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE.
RC SPECIES=Human; TISSUE=Brain;
RX MEDLINE=82231946; PubMed=7093203;
RA Sasagawa T., Ericsson L.H., Walsh K.A., Schreiber W.E., Fischer E.H.,
RA Titani K.;
RT "Complete amino acid sequence of human brain calmodulin.";
RL Biochemistry 21:2565-2569(1982).
RN [7]
RP SEQUENCE.
RC SPECIES=Rabbit; TISSUE=Skeletal muscle;
RX MEDLINE=81138220; PubMed=7202416;
RA Grand R.J.A., Shenolikar S., Cohen P.;
RT "The amino acid sequence of the delta subunit (calmodulin) of rabbit
RT skeletal muscle phosphorylase kinase.";
RL Eur. J. Biochem. 113:359-367(1981).
RN [8]
RP SEQUENCE.
RC SPECIES=Bovine; TISSUE=Brain;
RA Kasai H., Kato Y., Isobe T., Kawasaki H., Okuyama T.;
RT "Determination of the complete amino acid sequence of calmodulin
RT (phenylalanine-rich acidic protein II) from bovine brain.";
RL Biomed. Res. 1:248-264(1980).
RN [9]
RP SEQUENCE.
RC SPECIES=Bovine; TISSUE=Brain;
RX MEDLINE=80094551; PubMed=7356670;
RA Watterson D.M., Sharief F., Vanaman T.C.;
RT "The complete amino acid sequence of the Ca2+-dependent modulator
RT protein (calmodulin) of bovine brain.";
RL J. Biol. Chem. 255:962-975(1980).
RN [10]
RP SEQUENCE.
RC SPECIES=Bovine; TISSUE=Uterus;
RA Grand R.J.A., Perry S.V.;
RT "The amino acid sequence of the troponin C-like protein (modulator
RT protein) from bovine uterus.";
RL FEBS Lett. 92:137-142(1978).
RN [11]
RP SEQUENCE OF 38-60.
RC SPECIES=Bovine;
RX MEDLINE=89064822; PubMed=3058479;
RA Pribilla I., Krueger H., Buchner K., Otto H., Schiebler W.,
RA Tripier D., Hucho F.;
RT "Heat-resistant inhibitors of protein kinase C from bovine brain.";
RL Eur. J. Biochem. 177:657-664(1988).
RN [12]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=88257100; PubMed=3384819;
RA Bender P.K., Dedman J.R., Emerson C.P.;
RT "The abundance of calmodulin mRNAs is regulated in phosphorylase
RT kinase-deficient skeletal muscle.";
RL J. Biol. Chem. 263:9733-9737(1988).
RN [13]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=90006775; PubMed=2551780;
RA Danchin A., Sezer O., Glaser P., Chalon P., Caput D.;
RT "Cloning and expression of mouse-brain calmodulin as an activator of
RT Bordetella pertussis adenylate cyclase in Escherichia coli.";
RL Gene 80:145-149(1989).
RN [14]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=BALB/c; TISSUE=Brain;
RA Kato K.;
RT "A collection of cDNA clones with specific expression patterns in
RT mouse brain.";
RL Eur. J. Neurosci. 2:704-711(1991).
RN [15]
RP SEQUENCE.
RC SPECIES=Rat; TISSUE=Testis;
RX MEDLINE=78066877; PubMed=201628;
RA Dedman J.R., Jackson R.L., Schreiber W.E., Means A.R.;
RT "Sequence homology of the Ca2+-dependent regulator of cyclic
RT nucleotide phosphodiesterase from rat testis with other Ca2+-binding
RT proteins.";
RL J. Biol. Chem. 253:343-346(1978).
RN [16]
RP SEQUENCE FROM N.A.
RC SPECIES=Rat; TISSUE=Brain;
RX MEDLINE=87246077; PubMed=2885164;
RA Sherbany A.A., Parent A.S., Brosius J.;
RT "Rat calmodulin cDNA.";
RL DNA 6:267-272(1987).
RN [17]
RP SEQUENCE FROM N.A.
RC SPECIES=Rat; TISSUE=Brain;
RX MEDLINE=87226204; PubMed=3035194;
RA Nojima H., Hirofumi S.;
RT "Structure of a gene for rat calmodulin.";
RL J. Mol. Biol. 193:439-445(1987).
RN [18]
RP SEQUENCE FROM N.A.
RC SPECIES=Rat;

```
RX   MEDLINE=87257889; PubMed=3037336;
RA   Nojima H., Kishi K., Sokabe H.;
RT   "Multiple calmodulin mRNA species are derived from two distinct
RT   genes.";
RL   Mol. Cell. Biol. 7:1873-1880(1987).
RN   [19]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Rat; STRAIN=SHR;
RX   MEDLINE=89362474; PubMed=2527998;
RA   Nojima H.;
RT   "Structural organization of multiple rat calmodulin genes.";
RL   J. Mol. Biol. 208:269-282(1989).
RN   [20]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Chicken;
RX   MEDLINE=84008199; PubMed=6137485;
RA   Putkey J.A., Ts'Ui K.F., Tanaka T., Lagace L., Stein J.P., Lai E.C.,
RA   Means A.R.;
RT   "Chicken calmodulin genes. A species comparison of cDNA sequences and
RT   isolation of a genomic clone.";
RL   J. Biol. Chem. 258:11864-11870(1983).
RN   [21]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Chicken;
RX   MEDLINE=85104969; PubMed=2981850;
RA   Simmen R.C.M., Tanaka T., Ts'Ui K.F., Putkey J.A., Scott M.J.,
RA   Lai E.C., Means A.R.;
RT   "The structural organization of the chicken calmodulin gene.";
RL   J. Biol. Chem. 260:907-912(1985).
RN   [22]
RP   ERRATUM.
RC   SPECIES=Chicken;
RA   Simmen R.C.M., Tanaka T., Ts'Ui K.F., Putkey J.A., Scott M.J.,
RA   Lai E.C., Means A.R.;
RL   J. Biol. Chem. 262:4928-4929(1987).
RN   [23]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Chicken;
RA   Iida Y.;
RT   "cDNA sequences and molecular evolution of calmodulin genes of
RT   chicken and eel.";
RL   Bull. Chem. Soc. Jpn. 57:2667-2668(1984).
RN   [24]
RP   SEQUENCE FROM N.A.
RC   SPECIES=A.platyrhynchos;

  Query Match             52.1%;  Score 379.5;  DB 1;  Length 148;
  Best Local Similarity   51.7%;  Pred. No. 2.7e-18;
  Matches   75;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:||:
Db       1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGN 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | |||| ||| :     |::: ||| ||:||:|:|:  ||| | ||: | ||
Db      61 GTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARML 143
           :| ||||||:| ||:||||||| :|:
Db     121 VDEMIREADIDGDGQVNYEEFVQMM 145


RESULT 7
CALM_STIJA
ID   CALM_STIJA     STANDARD;      PRT;   148 AA.
AC   P21251;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin.
OS   Stichopus japonicus (Sea cucumber).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Holothuroidea; Aspidochirotacea; Aspidochirotida; Stichopodidae;
OC   Stichopus.
OX   NCBI_TaxID=7692;
RN   [1]
RP   SEQUENCE.
RA   Toda H., Abe Y., Yazawa M., Yagi K.;
RT   "Amino acid sequence of sea cucumber calmodulin.";
RL   Seikagaku 57:1037-1037(1985).
CC   -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC       ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC       CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC       PHOSPHATASES.
CC   -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC       SITES.
CC   -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR   PIR; JK0011; MCSFCU.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium-binding; Repeat; Methylation.
FT   MOD_RES       1      1       BLOCKED.
FT   MOD_RES     115    115       METHYLATION.
FT   CA_BIND      20     31       EF-HAND 1.
FT   CA_BIND      56     67       EF-HAND 2.
FT   CA_BIND      93    104       EF-HAND 3.
FT   CA_BIND     129    140       EF-HAND 4.
FT   VARIANT      78     78       D -> E.
FT   VARIANT      99     99       Y -> F.
SQ   SEQUENCE   148 AA;  16695 MW;  4653EA287472D1CA CRC64;

  Query Match             51.9%;  Score 378.5;  DB 1;  Length 148;
  Best Local Similarity   50.7%;  Pred. No. 3.2e-18;
  Matches   75;  Conservative   32;  Mismatches   38;  Indels    3;  Gaps    2;

Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:||:
Db       1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGN 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | |||| ||| :     |::: ||| ||:||:|:|:  ||| | ||: | ||
Db      61 GTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARMLAQE 146
           :| ||||||:| ||:||||||  |:  :
Db     121 VDEMIREADIDGDGQVNYEEFVTMMTSK 148


RESULT 8
CALM_ELEEL
ID   CALM_ELEEL     STANDARD;      PRT;   148 AA.
AC   P02594; Q90496;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin.
OS   Electrophorus electricus (Electric eel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Electrophoridae; Electrophorus.
OX   NCBI_TaxID=8005;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Electroplax;
RX   MEDLINE=83108962; PubMed=6185488;
RA   Lagace L., Chandra T., Woo S.L.C., Means A.R.;
RT   "Identification of multiple species of calmodulin messenger RNA using
RT   a full length complementary DNA.";
RL   J. Biol. Chem. 258:1684-1688(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
```

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RC   TISSUE=Electroplax;
RA   Iida Y.;
RT   "cDNA sequences and molecular evolution of calmodulin genes of
RT   chicken and eel.";
RL   Bull. Chem. Soc. Jpn. 57:2667-2668(1984).
RN   [3]
RP   SEQUENCE OF 92-113 FROM N.A.
RC   TISSUE=Electroplax;
RX   MEDLINE=81223873; PubMed=6941292;
RA   Munjaal R.P., Chandra T., Woo S.L.C., Dedman J.R., Means A.R.;
RT   "A cloned calmodulin structural gene probe is complementary to DNA
RT   sequences from diverse species.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:2330-2334(1981).
CC   -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC       ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC       CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC       PHOSPHATASES.
CC   -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC       SITES.
CC   -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00931; -; NOT_ANNOTATED_CDS.
DR   EMBL; M36168; AAA49236.1; -.
DR   EMBL; M17495; AAA49237.1; -.
DR   EMBL; M25058; AAA62797.1; -.
DR   PIR; A03022; MCEE.
DR   HSSP; P02593; 1CMG.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium-binding; Repeat.
FT   INIT_MET      0      0
FT   CA_BIND      20     31       EF-HAND 1.
FT   CA_BIND      56     67       EF-HAND 2.
FT   CA_BIND      93    104       EF-HAND 3.
FT   CA_BIND     129    140       EF-HAND 4.
FT   CONFLICT     92     92       F -> V (IN REF. 3; AAA62797).
FT   CONFLICT     95     95       D -> E (IN REF. 2 AND 3; AAA49237).
FT   CONFLICT    106    106       R -> G (IN REF. 2 AND 3; AAA49237).
FT   CONFLICT    109    109       M -> I (IN REF. 2 AND 3; AAA49237).
FT   CONFLICT    113    113       G -> A (IN REF. 3; AAA62797).
SQ   SEQUENCE   148 AA;  16678 MW;  464B950A496A83F7 CRC64;

  Query Match             51.8%;  Score 377.5;  DB 1;  Length 148;
  Best Local Similarity   50.3%;  Pred. No. 3.7e-18;
  Matches   73;  Conservative   31;  Mismatches   38;  Indels    3;  Gaps    1;

Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:|||  | ||:||| :||| ::: |:| :||:|: :|:|||:||:
Db       1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGN 60

Qy      62 GEISFQEFLTAARKARAGL---EDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | ||||   |        |::: ||| ||:||:|:|:  |||  |  ||: |  ||
Db      61 GTIDFPEFLTMMAKKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARML 143
           :| ||||||:| ||:|||||| :|:
Db     121 VDEMIREADIDGDGQVNYEEFVQMM 145


RESULT 9
CALM_DROME
ID   CALM_DROME     STANDARD;      PRT;   148 AA.
AC   P07181; Q9V3T4;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin.
GN   CAM OR CAL OR CG8472.
OS   Drosophila melanogaster (Fruit fly),
OS   Locusta migratoria (Migratory locust),
OS   Aplysia californica (California sea hare),
OS   Halocynthia roretzi (Sea squirt),
OS   Branchiostoma floridae (Florida lancelet) (Amphioxus), and
OS   Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227, 7004, 6500, 7729, 7739, 7740;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=D.melanogaster; STRAIN=Canton-S, and Oregon-R;
RX   MEDLINE=87203365; PubMed=3106931;
RA   Yamanaka M.K., Saugstad J.A., Hanson-Painton O., McCarthy B.J.,
RA   Tobin S.L.;
RT   "Structure and expression of the Drosophila calmodulin gene.";
RL   Nucleic Acids Res. 15:3335-3348(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=D.melanogaster;
RX   MEDLINE=88062687; PubMed=3119855;
RA   Smith V.L., Doyle K.E., Maune J.F., Munjaal R.P., Beckingham K.;
RT   "Structure and sequence of the Drosophila melanogaster calmodulin
RT   gene.";
RL   J. Mol. Biol. 196:471-485(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=D.melanogaster;
RX   MEDLINE=90294277; PubMed=2113585;
RA   Doyle K.E., Kovalick G.E., Lee E., Beckingham K.;
RT   "Drosophila melanogaster contains a single calmodulin gene. Further
RT   structure and expression studies.";
RL   J. Mol. Biol. 213:599-605(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   SPECIES=D.melanogaster; STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [5]
RP   SEQUENCE OF 1-140 FROM N.A.
RC   SPECIES=D.melanogaster;
RX   MEDLINE=87228266; PubMed=3035324;
RA   Beckingham K., Doyle K.E., Maune J.F.;
RT   "The calmodulin gene of Drosophila melanogaster.";
RL   Meth. Enzymol. 139:230-247(1987).
RN   [6]
RP   SEQUENCE.
RC   SPECIES=L.migratoria;
RA   Toda H.;
RL   Submitted (MAY-1988) to the PIR data bank.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   SPECIES=A.californica; TISSUE=Ganglion;
RX   MEDLINE=91080147; PubMed=2258931;
RA   Swanson M.E., Sturner S.F., Schwartz J.H.;
RT   "Structure and expression of the Aplysia californica calmodulin
RT   gene.";
RL   J. Mol. Biol. 216:545-553(1990).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   SPECIES=B.floridae;
RA   Karabinos A., Riemer D., Weber K.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   SEQUENCE FROM N.A.
RC   SPECIES=H.roretzi;
RX   MEDLINE=99196995; PubMed=10095116;
RA   Yuasa H.J., Yamamoto H., Takagi T.;
RT   "The structural organization of the ascidian, Halocynthia roretzi,
RT   calmodulin genes. The vicissitude of introns during the evolution of
RT   calmodulin genes.";
RL   Gene 229:163-169(1999).
RN   [10]
RP   SEQUENCE FROM N.A.
RC   SPECIES=H.roretzi, B.floridae, and B.lanceolatum;
RA   Yuasa H.J., Takagi T.;
RT   "Primary structure of Protochordate calmodulin.";
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [11]
RP   STRUCTURE BY NMR.
RC   SPECIES=D.melanogaster;
RX   MEDLINE=91369934; PubMed=1909892;
RA   Ikura M., Spera S., Barbato G., Kay L.E., Krinks M., Bax A.;
RT   "Secondary structure and side-chain 1H and 13C resonance assignments
RT   of calmodulin in solution by heteronuclear multidimensional NMR
RT   spectroscopy.";
RL   Biochemistry 30:9216-9228(1991).
RN   [12]
RP   STRUCTURE BY NMR.
RC   SPECIES=D.melanogaster;
RX   MEDLINE=92263094; PubMed=1585175;
RA   Ikura M., Clore G.M., Gronenborn A.M., Zhu G., Klee C.B., Bax A.;
RT   "Solution structure of a calmodulin-target peptide complex by
RT   multidimensional NMR.";
RL   Science 256:632-638(1992).
RN   [13]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC   SPECIES=D.melanogaster;
RX   MEDLINE=92042027; PubMed=1939171;
RA   Taylor D.A., Sack J.S., Maune J.F., Beckingham K., Quiocho F.A.;
RT   "Structure of a recombinant calmodulin from Drosophila melanogaster
RT   refined at 2.2-A resolution.";
RL   J. Biol. Chem. 266:21375-21380(1991).
CC   -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC       ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC       CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC       PHOSPHATASES.
CC   -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC       SITES.
CC   -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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CC   ---------------------------------------------------------------------
DR   EMBL; Y00133; CAA68327.1; -.
DR   EMBL; X05948; CAA29380.1; -.
DR   EMBL; X05949; CAA29381.1; -.
DR   EMBL; X05950; CAB51566.1; -.
DR   EMBL; X05951; CAA29383.1; -.
DR   EMBL; AE003823; AAF58542.1; -.
DR   EMBL; AE003823; AAF58543.1; -.
DR   EMBL; X56888; CAA40207.1; -.
DR   EMBL; X64653; -; NOT_ANNOTATED_CDS.
DR   EMBL; X64655; -; NOT_ANNOTATED_CDS.
DR   EMBL; Y09863; CAA70990.1; -.
DR   EMBL; Y09880; CAA71006.1; -.
DR   EMBL; AB018796; BAA33967.1; -.
DR   EMBL; AB003081; BAA19786.1; -.
DR   EMBL; AB003082; BAA19787.1; -.
DR   EMBL; AB003083; BAA19788.1; -.
DR   PIR; JK0010; MCLQ.
DR   PIR; S01173; MCFF.
DR   PIR; S13248; MCGAC.
DR   PDB; 4CLN; 15-JUL-92.
DR   PDB; 2BBM; 31-JAN-94.
DR   PDB; 2BBN; 31-JAN-94.
DR   FlyBase; FBgn0000253; Cam.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium-binding; Repeat; Methylation; 3D-structure.
FT   INIT_MET      0      0
FT   MOD_RES       1      1       BLOCKED (IN LOCUST).
FT   MOD_RES     115    115       METHYLATION (IN LOCUST).
FT   CA_BIND      20     31       EF-HAND 1.
FT   CA_BIND      56     67       EF-HAND 2.
FT   CA_BIND      93    104       EF-HAND 3.
FT   CA_BIND     129    140       EF-HAND 4.

  Query Match             51.5%;  Score 375.5;  DB 1;  Length 148;
  Best Local Similarity   50.7%;  Pred. No. 4.9e-18;
  Matches   75;  Conservative   31;  Mismatches   39;  Indels    3;  Gaps    2;

Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||:
Db       1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGN 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | ||||  ||| :     |::: ||| ||:||:| |:  |||  |  ||: |  ||
Db      61 GTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDEE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARMLAQE 146
           :| ||||||:| ||:||||||  |:  :
Db     121 VDEMIREADIDGDGQVNYEEFVTMMTSK 148


RESULT 10
CLM4_MOUSE
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ID   CLM4_MOUSE     STANDARD;      PRT;   148 AA.
AC   Q9JM83; Q9CR31; Q9D1E9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin 4 (Calcium-binding protein Dd112).
GN   CALM4 OR DD112.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ikegawa S., Nakamura Y.;
RT   "DD112, a novel mouse gene implicated in the early stage of ectopic
RT   ossification.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Tongue;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- FUNCTION: IMPLICATED IN THE EARLY STAGE OF ECTOPIC OSSIFICATION.
CC   -!- SIMILARITY: CONTAINS 3 EF-HAND CALCIUM-BINDING DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB036744; BAA95412.1; -.
DR   EMBL; AK009956; BAB26608.1; -.
DR   EMBL; AK009664; BAB26425.1; -.
DR   EMBL; AK003648; BAB22914.1; -.
DR   HSSP; P02593; 1CDM.
DR   MGD; MGI:1931464; Calm4.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001125; Recoverin.
DR   Pfam; PF00036; efhand; 4.
DR   PRINTS; PR00450; RECOVERIN.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 3.
DR   PROSITE; PS00018; EF_HAND; 3.
KW   Calcium-binding; Repeat.
FT   CA_BIND      21     32       EF-HAND 1 (POTENTIAL).
FT   CA_BIND      57     68       EF-HAND 2 (POTENTIAL).
FT   CA_BIND      93    104       EF-HAND 3 (POTENTIAL).
FT   CONFLICT      9      9       E -> V (IN REF. 2; BAB22914).
FT   CONFLICT    124    124       M -> V (IN REF. 2; BAB22914).
FT   CONFLICT    146    148       VEN -> I (IN REF. 1).
SQ   SEQUENCE   148 AA;  16767 MW;  2AE22BC738AD2F9D CRC64;
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  Query Match           50.9%;  Score 371;  DB 1;  Length 148;
  Best Local Similarity  51.4%;  Pred. No. 9.5e-18;
  Matches   74;  Conservative   29;  Mismatches   39;  Indels    2;  Gaps    1;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           |:   | || |::: ||:  | : :| |: :||| :| |||| |  |: |||::|:||
Db       1 MSHGFTKEEVAEFQAAFNRFDKNKDGHISVEELGDVMKQLGKNLPEKDLKALISKLDTDG 60

Qy      61 DGEISFQEFLTAARKARAG--LEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           ||:|||:|||||  | : |    :|:  |   ||:|||:||||||: ::: ||: | |||
Db      61 DGKISFEEFLTAIEKYKKGHRAGELRAVFNVLDQNGDGYITVDELKESLSKLGESLSQEE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARM 142
           |: ||| |||||||:| |||| |:
Db     121 LEDMIRVADVDQDGKVKYEEFVRL 144


RESULT 11
CALM_PHYIN
ID   CALM_PHYIN     STANDARD;      PRT;   148 AA.
AC   P27165;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin (CaM).
GN   CMD1 OR CALPI.
OS   Phytophthora infestans (Potato late blight fungus).
OC   Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC   Phytophthora.
OX   NCBI_TaxID=4787;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93229802; PubMed=8471792;
RA   Pieterse C.M., Verbakel H.M., Spaans J.H., Davidse L.C., Govers F.;
RT   "Increased expression of the calmodulin gene of the late blight
RT   fungus Phytophthora infestans during pathogenesis on potato.";
RL   Mol. Plant Microbe Interact. 6:164-172(1993).
CC   -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC       ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC       CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC       PHOSPHATASES.
CC   -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC       SITES.
CC   -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M83535; AAA21424.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium-binding; Repeat.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   CA_BIND      20     31       EF-HAND 1.
FT   CA_BIND      56     67       EF-HAND 2.
FT   CA_BIND      93    104       EF-HAND 3.
FT   CA_BIND     129    140       EF-HAND 4.
SQ   SEQUENCE   148 AA;  16693 MW;  5F7F7EDFCD0A46D4 CRC64;

  Query Match           50.7%;  Score 369.5;  DB 1;  Length 148;
  Best Local Similarity  50.3%;  Pred. No. 1.2e-17;
  Matches   73;  Conservative   32;  Mismatches   37;  Indels    3;  Gaps    2;
```

```
Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||:
Db       1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGN 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | ||||  ||| :     |::  ||: ||:||:| |:  |||  |  ||: |  ||
Db      61 GTIDFPEFLTMMARKMKDTDSEEEILEAFKVFDKDGNGFISAAELRHIMTNLGEKLTDEE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARML 143
           :| ||||||:| ||::|||||  :|:
Db     121 VDEMIREADIDGDGQINYEEFVKMM 145


RESULT 12
CALM_CHLRE
ID   CALM_CHLRE     STANDARD;      PRT;   162 AA.
AC   P04352;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin.
OS   Chlamydomonas reinhardtii.
OC   Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC   Chlamydomonadaceae; Chlamydomonas.
OX   NCBI_TaxID=3055;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89066752; PubMed=3198631;
RA   Zimmer W.E., Schloss J.A., Silflow C.D., Youngblom J., Watterson D.M.;
RT   "Structural organization, DNA sequence, and expression of the
RT   calmodulin gene.";
RL   J. Biol. Chem. 263:19370-19383(1988).
RN   [2]
RP   SEQUENCE.
RA   Lukas T.J., Wiggins M.E., Watterson D.M.;
RT   "Amino acid sequence of a novel calmodulin from the unicellular alga
RT   Chlamydomonas.";
RL   Plant Physiol. 78:477-483(1985).
CC   -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC       ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC       CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC       PHOSPHATASES.
CC   -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC       SITES.
CC   -!- MISCELLANEOUS: METHYLATION STATE OF K-118 MAY BE IMPORTANT IN THE
CC       QUANTITATIVE REGULATION OF PLANT NAD KINASE ACTIVITY. AMONG THE
CC       EUKARYOTIC CALMODULINS, ONLY THE CHLAMYDOMONAS AND DICTYOSTELIUM
CC       PROTEINS HAVE AN UNMETHYLATED LYSINE AT THIS POSITION, AND ONLY
CC       THESE PROTEINS CAN INCREASE (4- TO 6-FOLD) THE MAXIMAL ACTIVATION
CC       OF THIS ENZYME.
CC   -!- MISCELLANEOUS: THIS PROTEIN IS UNUSUAL AMONG EUKARYOTIC
CC       CALMODULINS IN HAVING AN 11-RESIDUE EXTENSION OF ITS CARBOXYL END.
CC   -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M20729; AAA33083.1; -.
DR   PIR; A03030; MCKM.
DR   HSSP; P02593; 1CDM.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium-binding; Repeat; Acetylation.
FT   INIT_MET      0      0
FT   MOD_RES       1      1       ACETYLATION.
FT   CA_BIND      23     34       EF-HAND 1.
FT   CA_BIND      59     70       EF-HAND 2.
FT   CA_BIND      96    107       EF-HAND 3.
FT   CA_BIND     132    143       EF-HAND 4.
SQ   SEQUENCE   162 AA;  18165 MW;  DD0779F5AE4AA7D2 CRC64;

  Query Match             50.7%;  Score 369.5;  DB 1;  Length 162;
  Best Local Similarity   51.7%;  Pred. No. 1.3e-17;
  Matches   74;  Conservative   31;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       4 ELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGDGE 63
           :|| |: |::|:||:  | ||:|||  :|||  ::: |:| :||:|: :|||||:||:|
Db       6 QLTEEQIAEFKEAFALFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMISEVDADGNGT 65

Qy      64 ISFQEFL-TAARKARA--GLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEELD 120
           | | |||   ||| :     ::|: ||: ||:||:| |:  |||  |  ||: | :||:|
Db      66 IDFPEFLMLMARKMKETDHEDELREAFKVFDKDGNGFISAAELRHVMTNLGEKLSEEEVD 125

Qy     121 AMIREADVDQDGRVNYEEFARML 143
           |||||||| ||:|||||| ||:
Db     126 EMIREADVDGDGQVNYEEFVRMM 148


RESULT 13
CALM_BLAEM
ID   CALM_BLAEM     STANDARD;      PRT;   148 AA.
AC   Q9HFY6;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin (CaM).
GN   CMD1.
OS   Blastocladiella emersonii.
OC   Eukaryota; Fungi; Chytridiomycota; Blastocladiales; Blastocladiaceae;
OC   Blastocladiella.
OX   NCBI_TaxID=4808;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21140061; PubMed=11244068;
RA   Simao R.C.G., Gomes S.L.;
RT   "Structure, expression, and functional analysis of the gene coding
RT   for calmodulin in the chytridiomycete Blastocladiella emersonii.";
RL   J. Bacteriol. 183:2280-2288(2001).
CC   -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC       ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC       CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC       PHOSPHATASES (By similarity).
CC   -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC       SITES.
CC   -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF264065; AAG31446.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium-binding; Repeat; Methylation.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   MOD_RES     115    115       METHYLATION (BY SIMILARITY).
FT   CA_BIND      20     31       EF-HAND 1.
FT   CA_BIND      56     67       EF-HAND 2.
FT   CA_BIND      93    104       EF-HAND 3.
FT   CA_BIND     129    140       EF-HAND 4.
```

```
SQ   SEQUENCE   148 AA;  16651 MW;  0887BFA32AD834B2 CRC64;

  Query Match           50.5%;  Score 368.5;  DB 1;  Length 148;
  Best Local Similarity   49.7%;  Pred. No. 1.4e-17;
  Matches   72;  Conservative   35;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|  :|:|||:||:
Db       1 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELLVMINEVDADGN 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | ||||  ||| :     |::: ||: ||:||:|:|:  ||| |  ||: | ::|
Db      61 GTIDFPEFLTMMARKMKDSDSEEEIKEAFKVFDKDGNGYISAAELRHVMTNLGEKLSEDE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARML 143
           :: |||||||| ||::||||| :|:
Db     121 VEEMIREADVDGDGQINYEEFVKMM 145


RESULT 14
CLM_PLEOS
ID   CLM_PLEOS      STANDARD;      PRT;   148 AA.
AC   O94739;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin (CaM).
GN   CMD1.
OS   Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Agaricales; Pleurotaceae; Pleurotus.
OX   NCBI_TaxID=5322;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Park I., Yim J.;
RT   "Structure and sequence of the calmodulin gene from Pleurotus
RT   ostreatus.";
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC       ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC       CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC       PHOSPHATASES (By similarity).
CC   -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC       SITES.
CC   -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U91642; AAD17455.1; -.
DR   EMBL; U91643; AAD17456.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium-binding; Repeat; Acetylation.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   CA_BIND      20     31       EF-HAND 1.
FT   CA_BIND      56     67       EF-HAND 2.
FT   CA_BIND      93    104       EF-HAND 3.
FT   CA_BIND     129    140       EF-HAND 4.
SQ   SEQUENCE   148 AA;  16693 MW;  CA5A2344770EF12C CRC64;

  Query Match           50.5%;  Score 368.5;  DB 1;  Length 148;
  Best Local Similarity   49.7%;  Pred. No. 1.4e-17;
  Matches   72;  Conservative   34;  Mismatches   36;  Indels    3;  Gaps    2;

Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|: |: :::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||:
Db       1 ADQLSEEQISEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGN 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | ||||  ||| |     |::: ||: ||:||:|:|:  ||| |  ||: | |
Db      61 GTIDFPEFLTMMARKMRDTDSEEEIKEAFKVFDKDGNGYISAAELRHVMTNLGEKLTDNE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARML 143
           :| |||||||| ||::||||| :|:
Db     121 VDEMIREADVDGDGQINYEEFVKMM 145


RESULT 15
CALM_PLECO
ID   CALM_PLECO     STANDARD;      PRT;   148 AA.
AC   P11120;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Calmodulin (CaM).
GN   CMD1.
OS   Pleurotus cornucopiae (Cornucopia mushroom).
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Agaricales; Pleurotaceae; Pleurotus.
OX   NCBI_TaxID=5321;
RN   [1]
RP   SEQUENCE.
RA   Toda H., Sakiyama F., Yokono T., Miura K., Nakamura T.;
RT   "Amino acid sequence of Pleurotus cornucopiae calmodulin.";
RL   Seikagaku 59:589-589(1987).
CC   -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC       ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CC       CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC       PHOSPHATASES.
CC   -!- PTM: UNLIKE OTHER CALMODULINS, LYS-115 IS NOT TRIMETHYLATED.
CC   -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC       SITES.
CC   -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
DR   PIR; JK0014; MCMRP.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
KW   Calcium-binding; Repeat; Acetylation.
FT   MOD_RES       1      1       ACETYLATION.
FT   CA_BIND      20     31       EF-HAND 1.
FT   CA_BIND      56     67       EF-HAND 2.
FT   CA_BIND      93    104       EF-HAND 3.
FT   CA_BIND     129    140       EF-HAND 4.
SQ   SEQUENCE   148 AA;  16707 MW;  CA5A3528A70EF12C CRC64;

  Query Match           50.4%;  Score 367.5;  DB 1;  Length 148;
  Best Local Similarity   49.0%;  Pred. No. 1.6e-17;
  Matches   71;  Conservative   35;  Mismatches   36;  Indels    3;  Gaps    2;

Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|: |: :::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||:
Db       1 ADQLSEEQISEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGN 60

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | ||||  ||| |     |::: ||: ||:||:|:|:  ||| |  ||: | |
Db      61 GTIDFPEFLTMMARKMRDTDSEEEIKEAFKVFDKDGNGYISAAELRHVMTNLGEKLTDNE 120

Qy     119 LDAMIREADVDQDGRVNYEEFARML 143
           :| ||||||:| ||::||||| :|:
Db     121 VDEMIREADIDGDGQINYEEFVKMM 145
```

Search completed: March 24, 2003, 17:44:27
Job time : 12 secs

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 24, 2003, 17:44:10 ; Search time 34 Seconds
(without alignments)
884.791 Million cell updates/sec

Title: US-10-031-403-1
Perfect score: 729
Sequence: 1 MAGELTPEEEAQYKKAFSAV.....DVDQDGRVNYEEFARMLAQE 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	384.5	52.7	149	4	Q96HK3	Q96hk3 homo sapien
2	383.5	52.6	149	5	Q95NR9	Q95nr9 metridium s
3	383.5	52.6	149	11	Q9D6G4	Q9d6g4 mus musculu
4	382.5	52.5	149	5	O02367	O02367 ciona intes
5	380.5	52.2	149	5	Q9UB37	Q9ub37 branchiosto
6	380.5	52.2	149	5	O96081	O96081 halocynthia
7	379.5	52.1	149	5	Q9GRJ1	Q9grj1 lumbricus r
8	379.5	52.1	149	5	O16305	O16305 caenorhabdi
9	379.5	52.1	149	13	Q9U6D3	Q9u6d3 myxine glut
10	378.5	51.9	149	13	O93410	O93410 gallus gall
11	377.5	51.8	149	5	O97341	O97341 suberites d
12	375.5	51.5	146	5	Q94801	Q94801 toxoplasma
13	375.5	51.5	156	5	Q8STF0	Q8stf0 strongyloce
14	373.5	51.2	149	10	Q40302	Q40302 macrocystis
15	373	51.2	152	4	Q13942	Q13942 homo sapien
16	370.5	50.8	149	5	Q95NI4	Q95ni4 halichondri
17	369.5	50.7	149	5	Q9XZP2	Q9xzp2 branchiosto
18	366.5	50.3	149	5	O96102	O96102 physarum po
19	365.5	50.1	149	3	Q8X187	Q8x187 paxillus in
20	363.5	49.9	136	13	Q98UH8	Q98uh8 clemmys jap
21	361.5	49.6	149	10	Q93VL8	Q93vl8 phaseolus v
22	360.5	49.5	149	10	Q9M6U0	Q9m6u0 brassica na
23	359.5	49.3	149	10	O49183	O49183 oryza sativ
24	359.5	49.3	149	10	O82018	O82018 mougeotia s
25	359.5	49.3	149	11	Q9D6P8	Q9d6p8 mus musculu
26	358.5	49.2	136	13	Q98SE9	Q98se9 clemmys jap
27	358.5	49.2	136	13	Q91972	Q91972 oryzias lat
28	358.5	49.2	149	10	Q43699	Q43699 zea mays (m
29	358.5	49.2	149	10	O49184	O49184 o calmoduli
30	357.5	49.0	149	10	Q9ZTV3	Q9ztv3 phaseolus v
31	355.5	48.8	148	10	Q9LDQ9	Q9ldq9 chara coral
32	355.5	48.8	149	10	Q43412	Q43412 bidens pilo
33	355.5	48.8	149	11	Q99K52	Q99k52 mus musculu
34	354.5	48.6	149	10	Q43698	Q43698 zea mays (m
35	354.5	48.6	149	10	O22641	O22641 zea mays (m
36	354.5	48.6	149	10	P94058	P94058 triticum ae
37	352.5	48.4	148	10	Q8W0Q0	Q8w0q0 stevia reba
38	352.5	48.4	149	10	Q42478	Q42478 solanum tub
39	352.5	48.4	149	10	Q9FJ05	Q9fj05 arabidopsis
40	351.5	48.2	149	10	Q9SDJ0	Q9sdj0 oryza sativ
41	351.5	48.2	149	10	Q39447	Q39447 capsicum an
42	348.5	47.8	134	5	O17501	O17501 branchiosto
43	348.5	47.8	150	10	O65347	O65347 apium grave
44	346.5	47.5	164	10	Q39708	Q39708 dunaliella
45	345.5	47.4	138	10	O15931	O15931 symbiodiniu

ALIGNMENTS

RESULT 1
Q96HK3
ID Q96HK3 PRELIMINARY; PRT; 149 AA.
AC Q96HK3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calmodulin 2 (phosphorylase kinase, delta).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLADDER;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC008437; AAH08437.1; -.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
KW Kinase.
SQ SEQUENCE 149 AA; 16836 MW; 6B5E82A8DE10727B CRC64;

Query Match 52.7%; Score 384.5; DB 4; Length 149;
Best Local Similarity 52.1%; Pred. No. 3e-24;
Matches 76; Conservative 32; Mismatches 35; Indels 3; Gaps 2;

```
Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
             :| | | |||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
```

```
Db    121 EVDQMIREADIDGDGQVNYEEFVQMM 146


RESULT 2
Q95NR9
ID   Q95NR9      PRELIMINARY;      PRT;   149 AA.
AC   Q95NR9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Calmodulin.
GN   CAM.
OS   Metridium senile (Brown sea anemone) (Frilled sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Metridiidae; Metridium.
OX   NCBI_TaxID=6116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yuasa H.J., Suzuki T., Yazawa M.;
RT   "Structural organization of lower marine nonvertebrates calmodulin
RT   genes.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB063183; BAB61796.1; -.
DR   EMBL; AB063181; BAB61794.1; -.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ   SEQUENCE   149 AA;  16838 MW;  6B44A8917FD5927B CRC64;

  Query Match             52.6%;  Score 383.5;  DB 5;  Length 149;
  Best Local Similarity   51.0%;  Pred. No. 3.7e-24;
  Matches   76;  Conservative   32;  Mismatches   38;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :     |::: ||| ||:||:| |:  ||| |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARMLAQE 146
           |:| ||||||:| ||:|||||| :|:  :
Db     121 EVDEMIREADIDGDGQVNYEEFVKMMTSK 149


RESULT 3
Q9D6G4
ID   Q9D6G4      PRELIMINARY;      PRT;   149 AA.
AC   Q9D6G4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Adult male hippocampus cDNA, RIKEN full-length enriched library,
DE   clone:2900055D23, full insert sequence.
GN   CALM1 OR CALM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=HIPPOCAMPUS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK013695; BAB28959.1; -.
DR   HSSP; P02593; 1AK8.
DR   MGD; MGI:88251; Calm1.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001125; Recoverin.
DR   Pfam; PF00036; efhand; 4.
DR   PRINTS; PR00450; RECOVERIN.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_3.
SQ   SEQUENCE   149 AA;  16851 MW;  6B4BC3FCDE10679B CRC64;

  Query Match             52.6%;  Score 383.5;  DB 11;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 3.7e-24;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :     |::: ||| ||:||:| |:  ||| |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFLQMM 146


RESULT 4
O02367
ID   O02367      PRELIMINARY;      PRT;   149 AA.
AC   O02367;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Calmodulin.
GN   CAM.
OS   Ciona intestinalis.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC   Phlebobranchia; Cionidae; Ciona.
OX   NCBI_TaxID=7719;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98394335; PubMed=9727352;
RA   Di Gregorio A., Villani M.G., Locascio A., Ristoratore F., Aniello F.,
RA   Branno M.;
RT   "Developmantal regulation and tissue-specific localization of
RT   calmodulin mRNA in the protochordate Ciona intestinalis.";
RL   Dev. Growth Differ. 40:387-394(1998).
DR   EMBL; Y13578; CAA73906.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ   SEQUENCE   149 AA;  16836 MW;  6B554EFDAFD2E27B CRC64;

  Query Match             52.5%;  Score 382.5;  DB 5;  Length 149;
  Best Local Similarity   51.7%;  Pred. No. 4.4e-24;
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  Matches   77;  Conservative   30;  Mismatches   39;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :     |::: ||| ||:||:| |:  ||| |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARMLAQE 146
           |:| |||||||| ||:|||||  |:  :
Db     121 EVDEMIREADVDGDGQVNYEEFVNMMTNK 149


RESULT 5
Q9UB37
ID   Q9UB37      PRELIMINARY;      PRT;   149 AA.
AC   Q9UB37;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Calmodulin 2.
GN   CAM2.
OS   Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7740;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20407449; PubMed=10948270;
RA   Karabinos A., Bhattacharya D.;
RT   "Molecular evolution of calmodulin and calmodulin-like genes in the
RT   cephalochordate Branchiostoma.";
RL   J. Mol. Evol. 51:141-148(2000).
DR   EMBL; AJ133486; CAB38169.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001125; Recoverin.
DR   Pfam; PF00036; efhand; 4.
DR   PRINTS; PR00450; RECOVERIN.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ   SEQUENCE   149 AA;  16824 MW;  3AABA8917FDDB26D CRC64;

  Query Match             52.2%;  Score 380.5;  DB 5;  Length 149;
  Best Local Similarity   50.3%;  Pred. No. 6.5e-24;
  Matches   75;  Conservative   32;  Mismatches   39;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :     |::: ||| ||:||:| |:  ||| |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARMLAQE 146
           |:| |:||||:| ||:|||||  |:  :
Db     121 EVDEMVREADIDGDGQVNYEEFVEMMTSK 149


RESULT 6
O96081
ID   O96081      PRELIMINARY;      PRT;   149 AA.
AC   O96081;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Calmodulin B.
GN   CAM B.
OS   Halocynthia roretzi (Sea squirt).
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC   Stolidobranchia; Pyuridae; Halocynthia.
OX   NCBI_TaxID=7729;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99196995; PubMed=10095116;
RA   Yuasa H.J., Yamamoto H., Takagi T.;
RT   "The structural organization of the ascidian, Halocynthia roretzi,
RT   calmodulin genes. The vicissitude of introns during the evolution of
RT   calmodulin genes.";
RL   Gene 229:163-169(1999).
DR   EMBL; AB018797; BAA33968.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001125; Recoverin.
DR   Pfam; PF00036; efhand; 4.
DR   PRINTS; PR00450; RECOVERIN.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ   SEQUENCE   149 AA;  16841 MW;  9E5EECD47FC703CA CRC64;

  Query Match             52.2%;  Score 380.5;  DB 5;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 6.5e-24;
  Matches   76;  Conservative   30;  Mismatches   37;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:||| | ||:||| :||| ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKARA--GLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :     |::: ||| ||:||:| |:  ||| |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKETDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||  |:
Db     121 EVDEMIREADIDGDGQVNYEEFVTMM 146


RESULT 7
Q9GRJ1
ID   Q9GRJ1      PRELIMINARY;      PRT;   149 AA.
AC   Q9GRJ1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Calmodulin.
GN   CALMODULIN.
OS   Lumbricus rubellus (Humus earthworm).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC   Lumbricina; Lumbricidae; Lumbricus.
OX   NCBI_TaxID=35632;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sturzenbaum S.R., Manova A., Morgan A.J., Kille P., Schaffner W.,
RA   Georgiev O.;
RT   "Earthworm cDNAs.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ291615; CAC14791.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001125; Recoverin.
DR   Pfam; PF00036; efhand; 4.
DR   PRINTS; PR00450; RECOVERIN.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_3.
SQ   SEQUENCE   149 AA;  16841 MW;  6B44BFA17FC7027B CRC64;

  Query Match             52.1%;  Score 379.5;  DB 5;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 7.8e-24;
  Matches   76;  Conservative   30;  Mismatches   37;  Indels    3;  Gaps    2;
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Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :|||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :    |::: ||| ||:||:| |:  ||| |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||  |:
Db     121 EVDEMIREADIDGDGQVNYEEFVTMM 146


RESULT 8
O16305
ID   O16305      PRELIMINARY;      PRT;   149 AA.
AC   O16305;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   T21H3.3 protein.
GN   T21H3.3 OR CMD-1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=94150718; PubMed=7906398;
RA   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA   Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA   Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA   Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA   Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA   Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
RA   Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA   Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA   Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA   Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Scheet P.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Kraev A., Gazzotti P.;
RT   "Expression and functional characterization of calmodulin from
RT   Caenorhabditis elegans.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF016429; AAB65364.1; -.
DR   EMBL; AJ132193; CAA10601.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ   SEQUENCE   149 AA;  16824 MW;  6B40B8917FC7027B CRC64;

  Query Match             52.1%;  Score 379.5;  DB 5;  Length 149;
  Best Local Similarity   52.1%;  Pred. No. 7.8e-24;
  Matches   76;  Conservative   30;  Mismatches   37;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :|||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :    |::: ||| ||:||:| |:  ||| |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||  |:
Db     121 EVDEMIREADIDGDGQVNYEEFVTMM 146


RESULT 9
Q9U6D3
ID   Q9U6D3      PRELIMINARY;      PRT;   149 AA.
AC   Q9U6D3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Calmodulin.
GN   CAM.
OS   Myxine glutinosa (Atlantic hagfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
OC   Myxinidae; Myxininae; Myxine.
OX   NCBI_TaxID=7769;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=INTESTINE;
RA   White G.P., Cunningham C.;
RT   "Characterization of a cDNA encoding calmodulin from the Atlantic
RT   hagfish (Myxine glutinosa).";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF187305; AAD56955.1; -.
DR   HSSP; P02593; 1CMG.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001125; Recoverin.
DR   Pfam; PF00036; efhand; 4.
DR   PRINTS; PR00450; RECOVERIN.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_3.
SQ   SEQUENCE   149 AA;  16836 MW;  8BA5C31CD4BA78DB CRC64;

  Query Match             52.1%;  Score 379.5;  DB 13;  Length 149;
  Best Local Similarity   51.4%;  Pred. No. 7.8e-24;
  Matches   75;  Conservative   33;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :|||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVNADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | |||| ||| :    |::: ||| ||:||:|:|:  ||| |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||:|||||| :|:
Db     121 EVDEMIREADIDGDGQVNYEEFVQMM 146


RESULT 10
O93410
ID   O93410      PRELIMINARY;      PRT;   149 AA.
AC   O93410;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Calmodulin.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90281977; PubMed=2162134;
RA   Van Eldik L.J., Zimmer W.E., Barger S.W., Watterson D.M.;
RT   "Perturbation of the calmodulin system in transformed cells.";
RL   Adv. Exp. Med. Biol. 269:111-120(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Van Eldik L.J., Zimmer W.E., Barger S.W., Watterson D.M.;
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF081672; AAC31608.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ   SEQUENCE   149 AA;  16852 MW;  6B4BC3FCD550C67B CRC64;

  Query Match             51.9%;  Score 378.5;  DB 13;  Length 149;
  Best Local Similarity   50.7%;  Pred. No. 9.5e-24;
  Matches   74;  Conservative   34;  Mismatches   35;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           ::| ||||:|:| ||:|||||| :|:
Db     121 QVDEMIRESDIDGDGQVNYEEFVQMM 146


RESULT 11
O97341
ID   O97341      PRELIMINARY;      PRT;   149 AA.
AC   O97341;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Calmodulin.
OS   Suberites domuncula (Sponge).
OC   Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC   Hadromerida; Suberitidae; Suberites.
OX   NCBI_TaxID=55567;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99191695; PubMed=10091595;
RA   Wimmer W., Perovic S., Kruse M., Schroeder H.C., Krasko A., Batel R.,
RA   Mueller W.E.G.;
RT   "Origin of the integrin-mediated signal transduction:Functional
RT   studies with cell cultures from the sponge Suberites domuncula.";
RL   Eur. J. Biochem. 260:156-165(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Schuetze J., Reis Custodio M., Efremova S.M., Mueller I.M.,
RA   Mueller W.E.G.;
RT   "Evolutionary relationship of metazoa within the eukaryotes based on
RT   molecular data from porifera.";
RL   Proc. R. Soc. Lond., B, Biol. Sci. 0:0-0(0).
DR   EMBL; Y18166; CAA77069.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001125; Recoverin.
DR   Pfam; PF00036; efhand; 4.
DR   PRINTS; PR00450; RECOVERIN.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ   SEQUENCE   149 AA;  16798 MW;  83EE891A0ACA828F CRC64;

  Query Match             51.8%;  Score 377.5;  DB 5;  Length 149;
  Best Local Similarity   51.0%;  Pred. No. 1.1e-23;
  Matches   76;  Conservative   30;  Mismatches   40;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDTDG 60

Qy      61 DGEISFQEFLT-AARKARA--GLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKETDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARMLAQE 146
           |:| |||||| | ||:||||||  |:  :
Db     121 EVDEMIREADTDGDGQVNYEEFVGMMTSK 149


RESULT 12
Q94801
ID   Q94801      PRELIMINARY;      PRT;   146 AA.
AC   Q94801;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Calmodulin (Fragment).
OS   Toxoplasma gondii.
OC   Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC   Toxoplasma.
OX   NCBI_TaxID=5811;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RH;
RX   MEDLINE=99270320; PubMed=10340495;
RA   Seeber F., Beuerle B., Schmidt H.H.H.W.;
RT   "Cloning and functional expression of the Calmodulin gene from
RT   Toxoplasma gondii.";
RL   Mol. Biochem. Parasitol. 99:295-299(1999).
DR   EMBL; Y08373; CAA69660.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001125; Recoverin.
DR   Pfam; PF00036; efhand; 4.
DR   PRINTS; PR00450; RECOVERIN.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_4.
FT   NON_TER     146    146
SQ   SEQUENCE   146 AA;  16474 MW;  E7D37EC3A9ACE7AF CRC64;

  Query Match             51.5%;  Score 375.5;  DB 5;  Length 146;
  Best Local Similarity   52.1%;  Pred. No. 1.6e-23;
  Matches   76;  Conservative   30;  Mismatches   37;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |:|  ||: ||:||:|:|:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTLMARKMKDTDTEEELIEAFKVFDRDGNGFISAAELRHVMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| |||||||| ||::||||| :|:
Db     121 EVDEMIREADVDGDGQINYEEFVKMM 146


RESULT 13
Q8STF0
ID   Q8STF0      PRELIMINARY;      PRT;   156 AA.
AC   Q8STF0;
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DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Calmodulin.
GN   EXCAM OR CAM.
OS   Strongylocentrotus intermedius.
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC   Strongylocentrotus.
OX   NCBI_TaxID=7667;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=INTERALVEOLAR MUSCLE;
RA   Yuasa H.J., Yazawa M.;
RT   "Genomic structure of calmodulin from the sea urchin,
RT   Strongylocentrotus intermedius: Molecular evolution of deuterostomian
RT   calmodulin genes.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB081567; BAB89359.1; -.
DR   EMBL; AB081569; BAB89361.1; -.
SQ   SEQUENCE   156 AA;  17596 MW;  4CF85F0398030023 CRC64;

  Query Match             51.5%;  Score 375.5;  DB 5;  Length 156;
  Best Local Similarity   50.7%;  Pred. No. 1.8e-23;
  Matches   75;  Conservative   31;  Mismatches   39;  Indels    3;  Gaps    2;

Qy       2 AGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDGD 61
           | :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||:
Db       9 ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGN 68

Qy      62 GEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQEE 118
           | | | ||||  ||| :     |::: ||| ||:||:| |:  |||  |  ||: |  ||
Db      69 GTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGFISAAELRHVMTNLGEKLTDEE 128

Qy     119 LDAMIREADVDQDGRVNYEEFARMLAQE 146
           :| ||||||:| ||:||||||  |:  :
Db     129 VDEMIREADIDGDGQVNYEEFVTMMTSK 156


RESULT 14
Q40302
ID   Q40302      PRELIMINARY;      PRT;   149 AA.
AC   Q40302;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Calmodulin.
GN   CALMODULIN.
OS   Macrocystis pyrifera (Giant kelp).
OC   Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Lessoniaceae;
OC   Macrocystis.
OX   NCBI_TaxID=35122;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Love J., Oliver I.R., Trewavas A.J.;
RT   "The nucleotide sequence of Macrocystis pyrifera calmodulin cDNA.";
RL   Plant Physiol. 108:1748-1748(1995).
DR   EMBL; X85091; CAA59418.1; -.
DR   HSSP; P02593; 1AK8.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ   SEQUENCE   149 AA;  16809 MW;  7260207B676F9060 CRC64;

  Query Match             51.2%;  Score 373.5;  DB 10;  Length 149;
  Best Local Similarity   50.7%;  Pred. No. 2.4e-23;
  Matches   74;  Conservative   32;  Mismatches   37;  Indels    3;  Gaps    2;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSDG 60
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:||
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60

Qy      61 DGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPLPQE 117
           :| | | ||||  ||| :     |::  ||: ||:||:| |:  |||  |  ||: |  |
Db      61 NGTIDFPEFLTMMARKMKDTDSEEEIIEAFKVFDKDGNGFISAAELRHIMTNLGEKLTDE 120

Qy     118 ELDAMIREADVDQDGRVNYEEFARML 143
           |:| ||||||:| ||::||||| :|:
Db     121 EVDEMIREADIDGDGQINYEEFVKMM 146


RESULT 15
Q13942
ID   Q13942      PRELIMINARY;      PRT;   152 AA.
AC   Q13942;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Calmodulin.
GN   CAMIII.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=91027929; PubMed=2223880;
RA   Koller M., Schnyder B., Strehler E.E.;
RT   "Structural organization of the human CaMIII calmodulin gene.";
RL   Biochim. Biophys. Acta 1087:180-189(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=93237314; PubMed=8476923;
RA   Koller M., Strehler E.E.;
RT   "Functional analysis of the promoters of the human CaMIII calmodulin
RT   gene and of the intronless gene coding for a calmodulin-like
RT   protein.";
RL   Biochim. Biophys. Acta 1163:1-9(1993).
DR   EMBL; X52606; CAA36839.1; -.
DR   EMBL; X52607; CAA36839.1; JOINED.
DR   EMBL; X52608; CAA36839.1; JOINED.
DR   HSSP; P02593; 1CFC.
DR   InterPro; IPR002048; EF-hand.
DR   Pfam; PF00036; efhand; 4.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_3.
SQ   SEQUENCE   152 AA;  17163 MW;  E86F18345358E54E CRC64;

  Query Match             51.2%;  Score 373;  DB 4;  Length 152;
  Best Local Similarity   51.0%;  Pred. No. 2.7e-23;
  Matches   76;  Conservative   32;  Mismatches   35;  Indels    6;  Gaps    3;

Qy       1 MAGELTPEEEAQYKKAFSAVDTDGNGTINAQELGAALKATGKNLSEAQLRKLISEVDSD- 59
           || :|| |: |::|:|||  | ||:|||  :|||  ::: |:| :||:|: :|:|||:|
Db       1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADD 60

Qy      60 --GDGEISFQEFLT-AARKAR--AGLEDLQVAFRAFDQDGDGHITVDELRRAMAGLGQPL 114
             |:| | | ||||  ||| :     |::: ||| ||:||:|:|:  |||  |  ||: |
Db      61 LPGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKL 120

Qy     115 PQEELDAMIREADVDQDGRVNYEEFARML 143
           ||:| ||||||:| ||:|||||| :|:
Db     121 TDEEVDEMIREADIDGDGQVNYEEFVQMM 149


Search completed: March 24, 2003, 17:45:12
Job time : 37 secs
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